

Query Match	100.0%	Score 1851;	DB 19;	Length 1851;
Best Local Similarity	100.0%	Pred. No. 2.6e-288;	Mismatches 0;	Indels 0;
Matches 1851;	Conservative 0;	Indels 0;	Gaps 0;	;
Qy	1	CCATCGGATCACTCATGTTGACAGCTTATCATGATAAGCTTACTTTCGAATCAGG 60		
Db	1	CCATCGGATCACTCATGTTGACAGCTTATCATGATAAGCTTACTTTCGAATCAGG 60		
Qy	61	TCTATCTTGAACAGCAGAACATAGATAGGGCATGGAGATTACCGAGAACATATGA 120		
Db	61	TCTATCTTGAACAGCAGAACATAGATAGGGCATGGAGATTACCGAGAACATATGA 120		
Qy	121	ACGTTATACTCACATCAGCGAATTCGGCAATTGATGACATGGAACTTAATTCAATCAAT 180		
Db	121	ACGTTATACTCACATCAGCGAATTCGGCAATTGATGACATGGAACTTAATTCAATCAAT 180		
Qy	181	TGTTTAACTAACAGCAACTAGATTGACAACTAATTCTCAACAAACCTTAATTCAACAA 240		
Db	181	TGTTTAACTAACAGCAACTAGATTGACAACTAATTCTCAACAAACCTTAATTCAACAA 240		
Qy	241	TTCAGGTAACTCCACCCAGCTTCATGTTACCGTAAGTAATGATAACTTACAAAA 300		
Db	241	TTCAGGTAACTCCACCCAGCTTCATGTTACCGTAAGTAATGATAACTTACAAAA 300		
Qy	301	CCCTGTTACATCAAGGTTTTCTTCTTCTGCTGTCATGAGTTACCATACCTTCTTCTATA 360		
Db	301	CCCTGTTACATCAAGGTTTTCTTCTGCTGTCATGAGTTACCATACCTTCTTCTATA 360		
Qy	361	TATTGACAACTAATTGACAACACTCTCAATTATTTCTGCTACTCAAGTTCTCTC 420		
Db	361	TATTGACAACTAATTGACAACACTCTCAATTATTTCTGCTACTCAAGTTCTCTC 420		
Qy	421	ATTGATAATAGCTTAATTCCACCATCACTCTCCACTCTCTCAACTCTCAT 480		
Db	421	ATTGATAATAGCTTAATTCCACCATCACTCTCCACTCTCTCAACTCTCAT 480		
Qy	481	CATCTCTCACTTTCTGTTGTTAACACATAATCAAAATCTTTCGGCTACTTACCGTCAACACTCTCAT 540		
Db	481	CATCTCTCACTTTCTGTTGTTAACACATAATCAAAATCTTTCGGCTACTTACCGTCAACACTCTCAT 540		
Qy	541	TGGCTACTGTGTCACCTTAATCCCTTATCATGCTCTTAAACTCATCTAT 600		
Db	541	TGGCTACTGTGTCACCTTAATCCCTTATCATGCTCTTAAACTCATCTAT 600		
Qy	601	ATAACATATTCTCATCCCTACTATTTCTGTTAAAGATAAAATAACTTCTTT 660		
Db	601	ATAACATATTCTCATCCCTACTATTTCTGTTAAAGATAAAATAACTTCTTT 660		
Qy	661	TTTTGTTTATTATAATAAAATTATAAAGTTAATGTTAATGTTTAAATAATCAATT 720		
Db	661	TTTTGTTTATTATAATAAAATTATAAAGTTAATGTTAATGTTTAAATAATCAATT 720		
Qy	721	TTATTCTATTATAGTTAGCTTATTTCTGTTGTTGTTAATTTGTTGAAATTAAC 780		
Db	721	TTATTCTATTATAGTTAGCTTATTTCTGTTGTTGTTAATTTGTTGAAATTAAC 780		
Qy	781	CTTTTAATCTGAGGAGAACCCAGATAAAATGGAGATAATTATGGAAACAAATA 840		
Db	781	CTTTTAATCTGAGGAGAACCCAGATAAAATGGAGATAATTATGGAAACAAATA 840		
Qy	841	AAAAAGTTGAGAAAATAGCTTATTCTGTCACAGAACCCGATTCAGCACTCTAGTTAG 960		
Db	841	AAAAAGTTGAGAAAATAGCTTATTCTGTCACAGAACCCGATTCAGCACTCTAGTTAG 960		
Qy	901	CGCAAGGAGTATTGTCACAGAACCCGATTCAGCACTCTGACTAACAATCT 900		
Db	901	CGCAAGGAGTATTGTCACAGAACCCGATTCAGCACTCTGACTAACAATCT 900		
Qy	961	TAAAAACCTTCAAAATAATATTCTGTTGTTGTTAATTTGTTGAAATGAT 1020		
Db	961	TAAAAACCTTCAAAATAATATTCTGTTGTTGTTAATTTGTTGAAATGAT 1020		
Qv	1021	TGAAAACCTGTTGATCAGCAACTTTTATCTTACCAATTATAATATAATGTTTCAGGGCCAAATT 1080		

bacterial DNA fragment (ABA76825-ABA76861) specific for the target bacterial species but ubiquitous for different strains, amplifying the nucleic acid and detecting the presence or amount of an amplified sequence as an indication of the presence or amount of the target bacterial species. The invention includes primers and probes, especially (ABA76861-ABA7684) against the target bacterial species, especially *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*, *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*, *H. influenzae*, *M. catarrhalis* and/or group A Streptococci producing exotoxin A gene spe A, suspected to be present in a sample which is obtained from human patients, animals, environment or food, and which consists of one or more bacterial colonies. Oligonucleotide probes and primers complementary to the bacterial genes encoding resistance to antibiotics such as bla (cem), bla (rob), bla (shv), aadB, aacC1, aacC2, aacC3, aacA4, mech, vanA, vanB, vanX, sara, aacA-aphD, vat, vga, msra, sul and/or int (ABA76985-ABA77001) are also useful to identify commonly encountered and clinically important resistance genes. The invention provides a rapid method of bacterial identification that can be achieved, which reduces the time currently required for the identification of pathogens in the clinical laboratory.

xx Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 other;

Query Match 99.2%; Score 1835.4; DB 22; Length 1837;

Best Local Similarity 99.9%; Pred. No. 8.3e-285; Matches 1836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

04 15 TCACTTTGACAGCTTATCATGATAAAGCTTACTTTTGAAAC 74
 04 1 TCACTTTGACAGCTTATCATGATAAAGCTTACTTTTGAAAC 60
 04 75 AGGTGACACATAGATTAGGGCATGGGATTACAGAACATGAACTGATACTCAC 134
 04 61 AGGTGACACATAGATTAGGGCATGGGATTACAGAACATGAACTGATACTCAC 120
 04 135 ATCAAGCAATGGCAATGATGACATTGGACATTCAATCAATTGTTACTAACAG 194
 04 121 ATCAAGCAATGGCAATGATGACATTGGACATTCAATCAATTGTTACTAACAG 180
 04 195 CAACTAGATTCACAACTTACCGTAAGTAACTCATACATCAAACTCC 254
 04 181 CAACTAGATTCACAACTTACCGTAAGTAACTCATACATCAAACTCC 240
 04 255 ACCAGCCTCCATCAATGCTACCGTAAGTAACTCATACATCAAACTCC 314
 04 241 ACCAGCCTCCATCAATGCTACCGTAAGTAACTCATACATCAAACTCC 300
 04 315 GGTTTTCTCTTGTCTGCTGATGAGTACCATACCTTCAATGACAACTAA 374
 04 301 GGTTTTCTCTTGTCTGCTGATGACATTCAATCAACAGTTAACTCATACAA 360
 04 375 ATGGACACATCAATGCTACCGTAAGTAACTCATACATCAAACTCC 434
 04 361 ATGGACACATCAATGCTACCGTAAGTAACTCATACATCAAACTCC 420
 04 435 AATTCCACCATCACTTCTCAACTTCAACTCTCAACTCTCACATTCT 494
 04 421 AATTCCACCATCACTTCTCAACTTCAACTCTCAACTCTCACATTCT 480
 04 495 TCGTTGGTAACACATATCAATCTCCACTTCAACTCTCAACTCTCAC 554
 04 481 TCCTGGTAAACATTAATCAATCTCCCTTCAACTCTCAACTCTCAC 540
 04 555 CCTAAATAACCCCTATCATGCTTCAACTCTCAACTCTCACATTCT 614
 04 541 CCTAAATAACCCCTATCATGCTTCAACTCTCAACTCTCACATTCT 600
 04 615 CCNCCTACCATCACTATGCTAAAGATAAAATACATGTTTTGTTATTAT 674
 04 601 CCTCCPACCATCTATGCTAAAGATAAAATACATGTTTTGTTATTAT 660
 04 675 AATAAAATTAAATAAACTTAATGTTTTAAAATATAACATTCTTCAAT 734
 04 661 AATAAAATTAAATAAACTTAATGTTTTAAAATATAACATTCTTCAAT 720
 04 735 GTTACGCTTTCATGTTGTTAGTAAATTTGGTGAATTGTTAACCTTTAAATCTAG 794
 04 721 GTTACGCTTTCATGTTGTTAGTAAATTTGGTGAATTGTTAACCTTTAAATCTAG 780
 04 795 AGGAGACCCAGATAAAATGGGAAATTATGCAACATAAAAGTATGAG 854
 04 781 AGGAGACCCAGATAAAATGGGAAATTATGCAACATAAAAGTATGAG 840
 04 855 AAAATGTTATTGTTAGTGCATCTGGACTAACATTCTGGTAAAGGTTATT 914
 04 841 AAAATGTTATTGTTAGTGCATCTGGACTAACATTCTGGTAAAGGTTATT 900
 04 915 GCTCAACAGAACCCGGTCAAGCCAAACTCAGATCTAGTTAGTTAGTTAGTCAAA 974
 04 901 GCTCAACAAACCCGAACTCAGATCTGGTAAAGTAAACCTCTAA 960
 04 975 AATATATTTCTTTCTTTATGAGGTGACCCCTGTTACGTTACGAACTGTGAT 1034
 04 961 AATATATTTCTTTCTTTATGAGGTGACCCCTGTTACGTTACGAACTGTGAT 1020
 04 1035 CAACTTTATCTCACCATTATAATATAATGTTAGTAAATTTAA 1094
 04 1021 CAACTTTATCTCAGTTTAAATATATGTTCTGGGCCAATTGATTA 1080
 04 1095 ACTGACTTAAGAACCCAGAGATGGCAACTTTAAGGATAAAAGCTGATATTAT 1154
 04 1001 ACTGAATTTAGACACAGATGGCAACTTTAAGGATAAAAGCTGATATTAT 1140
 04 1155 GGTGTAAGATAATTACCATCTCTGTATTATGTAAGGAAATGGAGTGCATGTAC 1214
 04 1141 GGTGTAAGATAATTACCATCTCTGTATTATGTAAGGAAATGGAGTGCATGTAC 1200
 04 1215 TACGGAGGGTACAAATCATGAGGGATTACCTGAAATTCTAAAGGATAGTCGTT 1274
 04 1201 TACGGAGGGTACAAATCATGAGGGATTACCTGAAATTCTAAAGGATAGTCGTT 1260
 04 1205 AAAGTATCATACATGATGGTATCCTAACGGCTTATCTTGTGAAATTTAAAGAT 1334
 04 1261 AAAGTATCATACATGATGGTATCCTAACGGCTTATCTTGTGAAATTTAAAGAT 1320
 04 1335 GTAUCGTGCAAGAAATTGAGCTATAAGTTGAGAAATCTACAGATAATAGGACTA 1394
 04 1321 GTAUCGTGCAAGAAATTGAGCTATAAGTTGAGAAATCTACAGATAATAGGACTA 1380
 04 1395 TATACTAATGGACCTCTTAATAATGAAACTGGTATATAAGTCTACCTAAACA 1454
 04 1381 TATACTAATGGACCTCTTAATAATGAAACTGGTATATAAGTCTACCTAAACA 1440
 04 1455 GAAAGTTTGGTTGATTTCCTGTGACCAAGAATTACTCATTAATCTCATTGTATG 1514
 04 1441 GAAAGTTTGGTTGATTTCCTGTGACCAACAGCTTACATGAAATCTCATCTATG 1500
 04 1515 ATATAAAAGATAATGAAACCGCTTACATGAAACAGCTTACATGAAATCTCATCTATG 1574
 04 1501 ATATAAAAGATAATGAAACCGCTTACATGAAACAGCTTACATGAAATCTCATCTATG 1560
 04 1575 ACCAAGTAACTCTTGGCTTGGCAACCTTACCTACTGCTGTTGATCTAACAA 1634
 04 1561 ACCAAGTAACTCTTGGCTTGGCAACCTTACCTACTGCTGTTGATCTAACAA 1620
 04 1635 AATTCTTATTAATGTAACACCGCTTACATGAAACAGCTTACATGAAATCTCATCTATG 1744
 04 1621 AATTCTTATTAATGTAACACCGCTTACATGAAACAGCTTACATGAAATCTCATCTATG 1680
 04 1695 GCTTACCCCTTAATGTTGCTTATGTTGCTTATCTAACCTTAAGGA 1654
 04 1681 GCTTACCCCTTAATGTTGCTTATGTTGCTTATCTAACCTTAAGGA 1740
 04 1755 TTGATGGTAACTCCCATTTTCGACAGACATCGTCGCTGCTAACACAAATCAT 1814
 04 1741 TTGATGGTAACTCCCATTTTCGACAGACATCGTCGCTGCTAACACAAATCAT 1800

Qy	1815	AGAGAGGAGCTTGTAGCTTAGCAACTATTATCGTC	1851
Db	1801	AGCAGGGCTTGTAGCTTAGCAACTATTATCGTC	1837
RESULT 5			
ID	AAZ51112	standard; DNA; 1837 BP.	
XX			
AC	AAZ51112;		
XX			
05-JUN-2000	(first entry)		
XX			
DE		Streptococcal pyrogenic exotoxin A (SPE-A) encoding DNA.	
XX			
KW		Superantigen toxin; SAG; Streptococcal pyrogenic exotoxin A; SPE-A; antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor; cytostatic; antibody; staphylococcal/streptococcal toxin; toxin; SPEA42; diagnosis; treatment; superantigen-associated bacterial infection; ds.	
XX			
OS		Streptococcus sp.	
Key		Location/Qualifiers	
PH		814..1569	
FT		/*tag- a	
FT		/product= "Streptococcal pyrogenic exotoxin A (SPE-A)"	
FT			
XX			
PN	W0200009154-A1.		
XX			
PD	24-FEB-2000.		
XX			
PF	13-AUG-1998;	98WO-US16766.	
XX			
PR	13-AUG-1998;	98WO-US16766.	
XX			
(REED-)	REED ARMY INST RES WALTER.		
XX			
PI	Ulrich RG, Olson MA, Bavari S;		
XX			
WPI	2000-224177/19.		
DR	P-PSDB; AAY70109.		
XX			
PT	Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections		
PT			
XX			
PS	Example 12; Page 92-94; 118pp; English.		
XX			
CC	The present sequence is the DNA encoding Streptococcal pyrogenic exotoxin A (SPE-A), a bacterial superantigen toxin (SAG), used for the formulation of SPE-A vaccines. SPEA42. The coding region of this SAG toxin is altered by site directed mutagenesis, introducing L42R mutation, that results in disruption of binding of the toxin to both the MHC class I or T-cell antigen receptor. SPEA has antibacterial and cytostatic activity. This sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections.		
XX			
SQ	Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 other;		
Query Match	99.0%	Score 1832.2; DB 21; Length 1837;	
Best Local Similarity	99.8%	Pred. No. 2.7e-285;	
Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	15	TCATGTTGACACCTTATCATCGATAACCTTACTTTTCGATAACGCTTATCCCTTGAAAC	74
Db	1	TCATGTTGACAGCTTATCATCGATAACGCTTACTTTTCGATAACGCTTATCCCTTGAAAC	60
Qy	75	AGGGCACACATGATGGCATGGGATATTACAGACAACTATGAGCTTATGACTCAC	134

QY	1215	TACCGAGGGTAAATCATGAGGGAAATCATTTAGAAATTCCTAAAGATACTGCTT	1274	PR XX PA (USSA) US SEC OF ARMY.	25-JUN-1997; 97US-0882431.
Db	1201	TACCGAGGGTAAATCATGAGGGAAATCATTTAGAAATTCCTAAAGATACTGCTT	1260	XX PI Ulrich RG, Olson MA, Bavari S;	
QY	1275	AAAGTCAATCGATGTTCAAGGCTATCATTTGAAACAAATAAAAATG	1334	XX WPI: 2002-546281/58.	
Db	1261	AAATGATCAATCGATGTTCAAGGCTATCATTTGAAACAAATAAAAATG	1320	DR DR P-PSDB; ABB79505.	
QY	1335	GTACTGTCAGAAATAGACTATAAGGTTAGAAATTCCTACAGATATAAGCAACTA	1394	XX Novel, isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases	
Db	1321	GTACTGTCAGAAATAGACTATAAGGTTAGAAATTCCTACAGATATAAGCAACTA	1380	PS PT PT XX Disclosure; Column 61-63; 46pp; English.	
QY	1395	TATCTAATGGACCTCTAAATGAAACTGGATATAAGTCTACATTAAGATAA	1454	XX CC The present sequence is the coding sequence of Streptococcus pyogenes vaccine SPa42. The vaccine differs from the native SPEA sequence by substitution of the Leu-42 residue by Arg. This mutation is expected to disrupt contact between the toxin and the HLA-DR receptor, reducing DR1 binding. SPa42 can be expressed as a recombinant protein in Escherichia coli as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SPa42 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen can be used to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multivalent vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSST-1 and SPEA is predicted to provide protective immunity against the majority of bacterial superantigen toxins.	
Db	1381	TATCTAATGGACCTCTAAATGAAACTGGATATAAGTCTACATTAAGATAA	1440	XX CC Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 other;	
QY	1455	GAAGTTTTGGTTGGATTTCCTCGAACAGAAATTCTCAATCTATCTATG	1514	Query Match 99.0%; Score 1832.2; DB 24; Length 1837; Best Local Similarity 99.8%; Pred. No. 2.7e-285; Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Db	1441	GAAGTTTTGGTTGGATTTCCTCGAACAGAAATTCTCAATCTATCTATG	1500	QY	
QY	1515	ATATATAAGATAATGAAACGCTGACTCAACACAACTGAACTCTACCA	1574	15 TCATGTTGACAGCTTATCATGATGAACTAGCTACTTTGCAATCAGGCTPATCCUTGAAAC 74	
Db	1501	ATATATAAGATAATGAAACGCTGACTCAACACAACTGAACTCTACCA	1560	DB 1 TCATGTTGACAGCTTATCATGATGAACTAGCTACTTTGCAATCAGGCTPATCCUTGAAAC 60	
QY	1575	ACCGATTAACCTTGTCTTGCACACTTACCTACTGCTGGATTAGAAATTATGC	1634	QY	
Db	1561	ACCAAGTAACCTTGTCTTGCACACTTACCTACTGCTGGATTAGAAATTATGC	1620	75 AGGTGCAACATAGATTGGCATGGATTAAGGAAACTATGAAACCTATACTAC 134	
QY	1635	AATTCCTTTAAATGTTAAACCGCICATTGATGAGGGTTTGTCTTATCTAAAGA	1694	DB 61 AGTGCACAACTATGATTGGCATGGATTAAGGAAACTATGAAACCTATACTAC 120	
Db	1621	AATTCCTTTAAATGTTAAACCGCICATTGATGAGGGTTTGTCTTATCTAAAGA	1680	QY	
QY	1695	GCTTAACTCTCTAAATGCTGCAAAATTTTAAATGTTGGAATTGTTCTPATTTGAT	1754	135 ATCACGGCAATGGCAATTGATGACATTGGAACTAAATTCATCAATTGTTACTAACAG 194	
Db	1681	GCTTAACTCTCTAAATGCTGCAAAATTTTAAATGTTGGAATTGTTCTPATTTGAT	1740	DB 121 ATCACGGCAATGGCAATTGATGACATTGGAACTAAATTCATCAATTGTTACTAACAG 180	
QY	1755	TGTATGGGTAAATCCCTATTTCGACACATACATCGTGCACCTCTAACACAAATCAT	1814	QY	
Db	1741	TGTATGGGTAAATCCCTATTTCGACACATACATCGTGCACCTCTAACACAAATCAT	1800	195 CAACTAGATGACAACTTATTCACAAACGTTAAATTAAACACATTCAAGTAACTCCC 254	
QY	1815	AGACGGAGCTGTAGCTTAGACACTTTATGCT	1851	DB 181 CAACTAGATGACAACTTATTCACAAACGTTAAATTAAACACATTCAAGTAACTCCC 240	
Db	1801	AGACGGAGCTGTAGCTTAGACACTTTATGCT	1837	QY	
RESULT 6					
BN84229					
ID	ABN84229	standard; cDNA; 1837 BP.			
XX	23-SEP-2002	(first entry)			
XX	Streptococcal	pyrogenic exotoxin A vaccine SPEA42 coding sequence.			
XX	DE				
XX	Exotoxin A; SPEA; SPa42; superantigen; antigen; toxin; vaccine;				
KW	attenuation; mutant; gene; ss.				
XX	Streptococcus	pyogenes.			
XX	Synthetic.				
XX	Key	Location/Qualifiers			
FT	814..1565				
FT	/*tag=				
FT	/product= "SPEA42"				
XX	US6399332-B1.				
PD	04-JUN-2002.				
XX	98US-0144776.				
XX	01-SEP-1998;				
XX	481 TCATGTTGTTGAACTACATAATCAATCTTCGTTTACGACTATCGTACTGTGTC	54			
XX	495 TCATGTTGTTGAACTACATAATCAATCTTCGTTTACGACTATCGTACTGTGTC	55			
Db	421 ATTCGACATCACCTCTCCACTCTCTCCACTCTCTCCACTCTCACCTC	50			

(I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, *Bordetella* sp., *Corynebacterium* sp., Enterobacteriaceae group, *Escherichia coli*, *Mycobacteriaceae* family, *Pseudomonads* group, *Streptococcus* sp., *Neisseria gonorrhoeae* and *Staphylococcus* sp.. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH0010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.

Sequence 756 BP; 297 A; 110 C; 118 G; 231 T; 0 other;

Query Match Score 40.8%; Score 754.4%; DB 22; Length 756;

Best Local Similarity 99.9%; Pred. No. 2.1e-112; Mismatches 0; Indels 1; Gaps 0;

Matches 755; Conservative 0; Fasta

Qy ATGGAAACATAAAAAAGTATGAAAGAAAATGGTATTGTTAGCTGACATTCT 887

Db 1 ATGGAAACATAAAAAAGTATGAAAGAAAATGGTATTGTTAGCTGACATTCT 60

Qy 888 GGACTAACATCTCCAGAGTTATGTCAGAACAGCCGATCAAGCCACTCAC 947

Db 61 GGACTAACATCTCCAGAGTTATGTCAGAACAGCCGATCAAGCCACTCAC 120

Qy 948 AGATCTAGTTAGTTAAACCTTCATAAAATATATTCTTTATGAGGTGACCCCTGT 1007

Db 121 AGATCTAGTTAGTTAAACCTTCATAAAATATTTCTTTATGAGGTGACCCCTGT 180

Qy 1008 ACTCGAGGAATGTGAATCTGTTGATCAACTTTATCTCACATTAAATAATGTT 1067

Db 181 ACTCGAGGAATGTGAATCTGTTGATCAACTTTATCTCACATTAAATAATGTT 240

Qy 1068 TCAGGGCCAATTATGATAAATAAAACGTAACTTGTAACTTGTAACTTGTAA 1127

Db 241 TCAGGGCCAATTATGATAAATAAAACGTAACTTGTAACTTGTAACTTGTAA 300

Qy 1128 TTAAGGATATAAAACCTGATATTATGGTGTAAATAATTACATGAAGGGAAATCAT 1187

Db 301 TTAAAGGATATAAAACCTGATATTATGGTGTAAATAATTACATGAAGGGAAATCAT 1247

Qy 1188 GAAAATCGAGAAGGGTGCATGATCTACGGGGTAAACAATCATGAAGGGAAATCAT 1247

Db 361 GAAAATCGAGAAGGGTGCATGATCTACGGGGTAAACAATCATGAAGGGAAATCAT 420

Qy 1248 TTGAAATTCTCAAAGAGTAACTCGTAAAGATAGTCACTGCTCAAGATTGACATAAGTTGA 1307

Db 421 TTGAAATTCTCAAAGAGTAACTCGTAAAGTCACTGCTCAAGATTGACATAAGTTGA 480

Qy 1308 TTGATATTGAACTATAAAATGTTGACTGCTCAAGATTGACATAAGTTGA 1367

Db 481 TTGATATTGAACTATAAAATGTTGACTGCTCAAGATTGACATAAGTTGA 540

Qy 1368 AAATATCTTCAAGATAAACTGAACTATAACTATGAACTACTGAACTCTGA 1427

Db 541 AAATATCTTCAAGATAAACTGAACTATAACTATGAACTCTGA 600

Qy 1428 TATATAAGTCTCATCTAACTGAAAGTGTGTTGACTGTTCTCTGACCA 1487

Db 601 TATATAAGTCTCATCTAACTGAAAGTGTGTTGACTGTTCTCTGACCA 660

Qy 1488 GAAATTACTCAATCTAAATATCTTGTAAAGATAATGAAACGTTGACTCAAAC 1547

Db 661 GAAATTACTCAATCTAAATATCTTGTAAAGATAACACCAAGTAA 1583

Db 721 ACRAGCCAAATTGAACTCTACCTAACACCAACTAA 56

Qy 1548 ACRAGCCAAATTGAACTCTACCTAACACCAAGTAA 1583

Db 681 ATTATAAAATGAACTCTACCTAACACCAACTAA 56

Qy 621 ACCTATCTATTGCTAAAGATAAAATACATTGTTTTGTTATTATAATAAAA 680

Db 681 ATTATAAAATGAACTCTACCTAACACCAACTAA 56

329 GTCACCACTCTAACAGATGAGTGTGACAAATCGAGTAATTCACTGGTTGATGG 388
 XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 PA

973 AAATATATATATTCTTCTTATGAGGTGACCTCTTACTACCGGAATCTGAATCTGTTG 1032
 XX Telford J, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 WPI; 2002-352536/38.

389 AGATATGAAAGTTTGTGATGATAATCATGAACTAACGTTAACATCTATAG 448
 PT New Streptococcus protein for the treatment or prevention of infecti
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 Claim 8; Page 4196-4488; 4525pp; English.

1033 ATCACTTTATCTACCATTTATATATATATGTTCAAGGGCAA-----ATTATG 1083
 XX
 449 ATCAATTCTATATTCTTGTACTTAAAGACACTAAGTGTAGGGATATTG 508
 PT
 PT
 PT
 XX
 1084 ATAAATTAAAATGAACTTAAGACCAAGAGTGGCAACTTTATTAAGGATAAACAGC 1143
 XX
 509 ATATGTTGAGCTGAATTAAACAAAGATTAGCTGATAATACAGATAATAGC 568 .
 XX

1144 TTGATATTGTTGAGTAAATTACCATCTGTTATTTATGGAAA----- 1192
 CC The invention relates to a protein (ABP25413-ABP30859) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococci
 CC (Streptococcus pyogenes), comprising one of 5433 sequences (SI), give
 CC the specification. The proteins have antibacterial and antiinflammato
 CC activity. (I), nucleic acids encoding (I), ABN6044 ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds
 CC (I). A composition comprising (I) or nucleic acid encoding (I) and
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nuclei
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 Streptococcus proteins.
 XX

569 TAGATGTTGGAGCTATTATTAACAGTTATTCTAAAGTGTAACTGAGCTA 628
 SQ Sequence 2155561 BP; 695741 A; 385320 C; 382958 G; 691542 T; 0 other
 DB

1193 -----TGGAAAGGAGTGCAGTATCTACGGAGGGTAACAAATCATG 1236
 CC Query Match 9.7%; Score 178.8; Pred. No. 5; 3e-20;
 CC Best Local Similarity 71.8%; Mismatches 92; Indels 0; Gaps
 CC Matches 234; Conservative 0;
 CC

629 TTAATTGCGATCAACTGACAAGACCTGTTATCTATGGTTAACTGAGCTA 688
 CC

1237 AGGGAACTATTGAAATTCTAAAGATAGTCGTTAAAGGATCAATCGATGGTATCC 1296
 CC

689 ATGAAACCAATTGATAATAGAACTTACTGTTGCGGATTGAGTTGTAATAA 748
 CC

1297 AAAGCTTATCATTGATAATGAACTAAAAATGTAACTGCTCAAGATTAGCT 1356
 CC

749 ATTATTAACTTGTGACGTAAACTTAAGGAAATGAGTTAGATT 808
 CC

1357 ATAAAGTTGAAATAATCTTACAGATAATAAAGCAACTATATACTAATGGACCTCTAAAT 1416
 CC

809 ACCTAACTGTCACTATTGGTCAAAATAAAACTCTATGAAATTACACTCGCCTT 868
 CC

1417 ATGAAACTGATATAAAGTTCATACCTTAAGGATAAGAAACTTTGGTTGATTTT 1476
 CC

869 ATGAAACGGGATATAATTATTTATA--GAAATGAAATGACCTTGGTACATGA 925
 CC

1477 TCCTGTAACAG-----ATTAACTCATCTAAATCTTAAAGATAAGATAATG 1530
 CC

926 TGCGTGACCAAGGATATAATTGCCAACTCTAAATTAAGATGACAAATA 985
 CC

1531 AAAGCTTGACTCAAACACAAGGCAAATGAAACTCTACCTAAACCAAGATA 1583
 CC

986 AAATGGTGTGATTAAAGATGTGAGATTGAAAGTTATCCTAACACAAAGAA 1038
 CC

RESULT 10.
 ABN71527_c
 ID ABN71527 standard; DNA; 2155561 BP.
 XX
 AC ABN71527;
 XX
 DT 02-JUL-2002 (first entry)

XX Streptococcus polynucleotide SEQ ID NO 10367.
 XX
 DE Streptococcus sp.
 XX
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
 XX
 OS Streptococcus sp.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.

RESULT 11
 AAZ51108
 ID AAZ51108 standard; DNA; 1712 BP.
 XX
 AC AC
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Mutant Staphylococcal enterotoxin B DNA for vaccine B2360210P.

XX	Superantigen toxin; SAg; Staphylococcal enterotoxin B; SEB; cytotoxic; antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor; antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant; treatment; superantigen-associated bacterial infection; B2360210P; ds.	Db
KW	Staphylococcus sp.	Qy
XX	Staphylococcus	Db
XX	Key	Qy
FT	Location/Qualifiers	Db
CDS	244..1044	Qy
FT	/*tag= a	Db
FT	/product= "Mutant Staphylococcal enterotoxin B"	Qy
FT	247..327	Db
FT	/*tag= b	Qy
FT	mat_Peptide	Db
FT	328..1041	Qy
FT	/*tag= c	Db
FT	label= "Mature_Staphylococcal_enterotoxin_B"	Qy
FT	/note= "Mutant sequence inclusive of ATG start codon"	Db
FT	/transl_except= (pos:502..504, aa:Asp)	Qy
FT	/transl_except= (pos:712..774, aa:Tyr)	Db
FT	/transl_except= (pos:901..903, aa:Gln)	Qy
FT	/transl_except= (pos:904..909, aa:Asn)	Db
FT	/transl_except= (pos:1012..1014, aa:Leu)	Qy
XX	WO200009154-A1.	Db
XX	PD 24-FEB-2000.	Qy
XX	PP 13-AUG-1998;	Db
XX	PR 13-AUG-1998;	Qy
XX	PR 98WO-US16766.	Db
XX	PA (REED-) REED ARMY INST RES WALTER.	Qy
XX	PI Ulrich RG, Olson MA, Bavari S;	Db
XX	DR WPI: 2000-224177/19.	Qy
XX	DR P-PSB; AAY70105.	Db
XX	PT Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections	Qy
XX	PS Claim 5; Page 79-81; 118PP; English.	Db
CC	The present sequence is the DNA encoding mutant Staphylococcal enterotoxin B (SEB), a bacterial superantigen toxin (SAg), used for the SAg toxin is altered by site directed mutagenesis, that results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SEB has antibacterial and cytotoxic activity. This sequence is useful for the production of SEB vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections.	Db
XX	Sequence 1712 BP; 597 A; 224 C; 256 G; 635 T; 0 other;	Qy
CC	Query Match 9.5%; Score 176.2; DB 21; Length 1712; Best Local Similarity 54.0%; Pred. No. 1.2e-19; Matches 547; Conservative 0; Mismatches 413; Indels 53; Gaps 7;	Db
CC	XX	RESULT 12
CC	XX	ABN84225
CC	XX	ID ABN84225 standard; cDNA: 1712 EP.
CC	XX	AC ABN84225;
CC	XX	DT 23-SEP-2002 (first entry)
CC	XX	DE Staphylococcal enterotoxin B vaccine, periplasmic (B899445P)
CC	XX	KW Enterotoxin B; superantigen; antigen; toxin; vaccine; B899445P;
CC	XX	KW attenuation; mutant; gene; ss.
CC	OS Staphylococcus sp.	Db
CC	986 ATATGGTTGATTCTAAGATGTGAAGTTGAACTGAGTTGATCTGACAAAGANA 1038	Qy

XX	Ulrich RG,	Olson MA,	Bavari S;
PI			
XX			
DR	2000-224177/19.		
DR	P-PSDB;	AAV70108.	
XX			
PT	Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections		
PT	Example 13: Page 89-90; 118pp; English.		
XX			
CC	The present sequence is the DNA encoding Staphylococcus enterotoxin C1 (SEc1), a bacterial superantigen toxin (Sag), used for the formulation of SEC1 vaccine SEC45. The coding region of this Sag toxin is altered by site directed mutagenesis, introducing L5R mutation, that results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SEC1 has antibacterial and cytostatic activity. This sequence is useful for the production of SEC1 vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections.		
XX			
SQ	Sequence 1095 BP; 434 A; 125 C; 186 G; 350 T; 0 other:		
Query	Match 8.9%	Score 164 6;	DB 21; Length 1095;
Best	Local Similarity 56.7%	Pred. No. 8.7e-18;	
Matches	381; Conservative 0; Mismatches 229; Indels 39; Gaps 4;		
Qy	973 ARAATATATTTCTTCTTATGAGGTGACCCGTACTCAGAGATGGAATCTGTG	1032	
Db	263 ARAATGAAAGTTTATATGATCATTATGATCATTATGCAACTTAAGTAACTGTAG	322	
Qy	1033 AYCAACTTTATCACCATTAAATATPAATGTTGAGG-----GCCAAATTTATG	1083	
Db	323 ATAAATTAGGCACAGTATTAAATTATPACATAGTGTATAAAACTGAAATATG	382	
Qy	1084 ATAAATTAAACCTGAACTTAAGAACCAAGAGATGCCAACCTTATTAAGGATAAAACG	1143	
Db	383 ACAAATGAAACAGAGTTAAATGAGGTATAGCAAAAGAGTACAAAGATGAATGAG	442	
Qy	1144 TGTATTTATGTTGAGAATATACCATCCTCTGTTTATTAT-----	1185	
Db	443 TGTATGTTGATGATCATTAAACTATGTAACAGCTTATTTTCATCCAAGATAATGTAG	502	
Qy	1186 GAAATATGCCAAAGGGTGCATGATTCAGGGGGTAAACAAATCATGAGGAATC	1245	
Db	503 GAAATTAGGGGCCAAACTGTATGTTGAGGAAATACAAACATGAGGAAC	562	
Qy	1246 ATTGAAATTCTCA-----AAAGATAGTCTGTTAAAGTATCAATCGATGGPATCCCCAA	1299	
Db	563 ACTTGTAAATGGGAACTTACAAATGTTACTTAAAGTTGATGAAATAAAAGAAACA	622	
Qy	1300 GCCTCATTTGATGATGAAACAATAAAATGGTAACYGTCAAGAATTAGCTATA	1359	
Db	623 CATTCTTGTAGTCAAATCTGATAGAAGTGTAAAGCTTAAAGTCAAGACTGACATAA	682	
Qy	1360 AGTTGAAATAATCTCAAGATAATAAGCAACTTATACATTAATGCGCTCTTCAAAATG	1419	
Db	683 AGCTTGGATTTTAAATTTAAATTTAAATTTAAATTTAAACCGCATACCTTGTGATGATGTC	7442	
Qy	1420 ARACTGGATATAAGGTTCACTTCTAGAATAAGAAAGTTTGGTTGATTTTCC	1479	
Db	743 APACAGGATATAAAAATTATGAAATAACCGCATACCTTGTGATGATGATGTC	802	
Qy	1480 CTGAACCG-----AATTTACTCATCTAAATCTTATGATATAAAAGATAATGAA	1533	
Db	803 CTGCACCAAGCGGATAAGTTGACCATCTAAATTTAAATGTCACAAAGATAAA	862	
Qy	1534 CGCTGACTAACACACAGCCAAATGTAACCTAACCCAGTA 1582		
Db	863 CGGTGATCTTAAAGTGTGAGAATGTCACCTAACCCAGTA 911		

WPI:	2000-224177/19.	RESULT 15
P-PSDB:	AAY70108.	ABN84228
ID:	ABN84228 standard	ABN84228
XX	CDNA: 1095 BP.	ABN84228;
AC		ABN84228;
XX		
DT	23-SEP-2002 (first entry)	
XX	Staphylococcal SEC-1 vaccine SEC45 coding sequence.	
DE		
XX	Enterotoxin C1; SEC-1; SEC45; superantigen; antigen; toxin;	
KW	vaccine; attenuation; mutant; gene; ss.	
OS	Staphylococcus sp.	
OS	Synthetic.	
XX		
FH	Location/Qualifiers	
Key		
CDS		
FT	*tag= a	
FT	/transl_except= (pos:736..738,aa: Phe)	
FT	/product= "SEC45"	
FT		

Db	323	ATAAATTAGGGCACATGATTAAATTAAACATTAACATTAACACTGATAAAACTGAAAATTATG	382
Qy	1084	ATAAAATTAACACTGAACTTAAGAACCAAGATGGCAACTTATTAGGATAAAAAACG	1143
Db	383	ACAAAGTGAACAGGTATTAAATGAAAGTCAAAAGATGAAAGTAGTAAAGATGAGTAG	442
Qy	1144	TGATPATTATGGTAGAAATTACACATCTGTATTAT-----	1185
Db	443	TTGATGTTATGGATCAAATTACATGTAACACTGTATTTTCATCAAGATAATGTAG	502
Qy	1186	GTGAAATGCGAAAGGAGTCATGATCATGGAGGGTAACAAATCATGAAGGGAAATC	1245
Db	503	GTAAAGTTACAGTGGCAAACCTGTATGTTAGGAATAACAAACATGAAGCAACC	562
Qy	1246	ATTTAGAAATTCTA-----AAAGATAGTCGTTAAAGTCAATCGATGGTTTCAAA	1299
Db	563	ACTTGATAATGGACATTACAAAATGACTTATAGAGTTATGAAATAAAAGAAACA	622
Qy	1300	GCCTATCATTGATGATGAAACAAATTAAAAATGTAAGTCAGTCAGAAATTAGCTATA	1359
b	623	CAATTCTTIGAAGTGCAACTGTAAGAAACTGTACAGCTCAAGAACATGACATAA	682
Qy	1360	AACTGAAATATCTACAGATAATAGCAACTATACTAAATGACCTTCTAAATATG	1419
Db	683	AAAGCTTGGAAATTTTAAATAAAACATTGATGAGTTAACAGTTCACCATATG	742
Qy	1420	AAACCTGATATAAAAGTCATACCTAAGATAAAAGAAACTTGTGATTITTTCC	1479
Db	743	AAACAGGATATAAAATTATGAAATAACGGCAATACTTGTGATGATGATGTC	802
Qy	1480	CTGAAACAG-----AATTACTCATCTAAATCTTATGATAAAAGATAATGAAA	1533
Db	803	CTGCACAGCGATAAGTTGACCAATCTAAATTTAATGATGTCACAGACAAATAAA	862
Qy	1534	CGCTTGACTGAACTAACAAAGCCAAATTGAACTTACCTAACCAACCAAGTA	1582
Db	863	CGGTGTTCTAAAGTGTGAAAGTAGTCAAGTCCACCTTACACAGAA	911

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A; Note: the nucleotide sequence was submitted to the EMBL Data Library	A; Accession: S18794	A; Status: nucleic acid sequence not shown; translation not shown
A; Status: nucleic acid sequence not shown; translation not shown	A; Molecule type: DNA	A; Residues: 1-236 <NE2>
A; Cross-references: EMBL:X61570; PIDN:CA443768.1; PID:947315	A; Cross-references: EMBL:X61572; PIDN:CA443770.1; PID:947333	A; Experimental source: strain MGAS491 isolate United Kingdom unassigned
A; Note: the nucleotide sequence was submitted to the EMBL Data Library	A; Note: the nucleotide sequence was submitted to the EMBL Data Library	A; Note: the nucleotide sequence was submitted to the EMBL Data Library
A; Accession: S18801	A; Accession: S18798	A; Accession: S18798
A; Status: nucleic acid sequence not shown; translation not shown	A; Molecule type: DNA	A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-236 <NE2>	A; Cross-references: EMBL:X61571; PID:947323; PIDN:CA443769.1; PID:9473	A; Experimental source: strain MGAS624 isolate Germany unassigned phage
A; Status: nucleic acid sequence not shown; translation not shown	A; Status: nucleic acid sequence not shown; translation not shown	A; Note: the nucleotide sequence was submitted to the EMBL Data Library
C; Superfamily: enterotoxin B	C; Superfamily: enterotoxin B	C; Superfamily: enterotoxin B
C; Keywords: exotoxin	C; Keywords: exotoxin	C; Keywords: exotoxin
F; 1-22/Domain: signal sequence (fragment) #status predicted <SIG>	F; 23-236/Product: exotoxin type A (fragment) #status predicted <MAT>	F; 23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
Query Match 9 KKMVFVVLVIFGLTISQEVFAQQDPDSQLHRSSVLKVNQNIYFLYEGDPVTHEN	Best Local Similarity 99.2%	Length 236;
Matches 234; Conservative 1; Mismatches 1; Indels 0; G	pred. No. 1.e-85;	DB 2;
Qy 9 DOLLSHLITVNGPYPDKLKTELKQEMATLFDKNDIYGVVEYHLCYLCENAE	DB 69 DOLLSHLITVNGPYPDKLKTELKQEMATLFDKNDIYGVVEYHLCYLCENAE	Qy 129 IYGGYNHEGNHLETKKIVVKVSIDGIOSLSDIETNKMMTAQELDYKVRKYL
Db 1 KKMVFVVLVIFGLTISQEVFAQQDPDSQLHRSSVLKVNQNIYFLYEGDPVTHEN	DB 61 DOLLSDLITVNGPYPDKLKTELKQEMATLFDKNDIYGVVEYHLCYLCENAE	Db 121 IYGGYNHEGNHLETKKIVVKVSIDGIOSLSDIETNKMMTAQELDYKVRKYL
Qy 129 IYGGYNHEGNHLETKKIVVKVSIDGIOSLSDIETNKMMTAQELDYKVRKYL	Qy 189 LYTGNSKSYKENGYIKRIPKNEKSFEDDFPEPEFTQSKYLMIKYDNEFLDSNTSOI	Qy 181 LYTGNSKSYKENGYIKRIPKNEKSFEDDFPEPEFTQSKYLMIKYDNEFLDSNTSOI
Db 121 IYGGYNHEGNHLETKKIVVKVSIDGIOSLSDIETNKMMTAQELDYKVRKYL	Db 181 LYTGNSKSYKENGYIKRIPKNEKSFEDDFPEPEFTQSKYLMIKYDNEFLDSNTSOI	Db 181 LYTGNSKSYKENGYIKRIPKNEKSFEDDFPEPEFTQSKYLMIKYDNEFLDSNTSOI

A: Residues: 1-236 <NEAD>	A: Cross-references: ENBL:X61562; NID:947299; PIDN:CAA43760.1; PID:947300
A: Cross-references: ENBL:X61563; NID:947301; PIDN:CAA43761.1; PID:947302	A: Experimental source: strain MGAS251 isolate California unassigned phage
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991	A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A: Accession: S18788	A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA	A: Residues: 1-236 <NEAD>
A: Residues: 1-236 <NEAD>	A: Cross-references: ENBL:X61564; NID:947305; PIDN:CAA43762.1; PID:947306
A: Cross-references: ENBL:X61564; NID:947305; PIDN:CAA43762.1; PID:947306	A: Experimental source: strain MGAS256 isolate Colorado unassigned phage
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991	A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A: Accession: S18790	A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA	A: Residues: 1-236 <NEAD>
A: Residues: 1-236 <NEAD>	A: Cross-references: ENBL:X61565; NID:947311; PIDN:CAA43763.1; PID:947312
A: Cross-references: ENBL:X61565; NID:947311; PIDN:CAA43763.1; PID:947312	A: Experimental source: strain MGAS285 isolate Yugoslavia unassigned phage
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991	A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A: Accession: S18791	A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA	A: Residues: 1-236 <NEAD>
A: Residues: 1-236 <NEAD>	A: Cross-references: ENBL:X61566; NID:947317; PIDN:CAA43764.1; PID:947318
A: Cross-references: ENBL:X61566; NID:947317; PIDN:CAA43764.1; PID:947318	A: Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991	A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A: Accession: S18792	A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA	A: Residues: 1-236 <NEAD>
A: Residues: 1-236 <NEAD>	A: Cross-references: ENBL:X61567; NID:947325; PIDN:CAA43765.1; PID:947326
A: Cross-references: ENBL:X61567; NID:947325; PIDN:CAA43765.1; PID:947326	A: Experimental source: strain MGAS496 isolate Germany unassigned phage
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991	A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A: Accession: S18793	C: Genetics:
A: Molecule type: DNA	A: Gene: speA2
A: Residues: 1-236 <NEAD>	C: Superfamily: enterotoxin B
A: Cross-references: ENBL:X61568; NID:947327; PIDN:CAA43766.1; PID:947327	C: Keywords: exotoxin
A: Cross-references: ENBL:X61568; NID:947327; PIDN:CAA43766.1; PID:947327	F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
A: Cross-references: ENBL:X61568; NID:947327; PIDN:CAA43766.1; PID:947327	F:23-236/Product: exotoxin type A (fragment) #status predicted <MAP>
Query Match	93 28; Score 1233; DB 2; Length 236;
Best Local Similarity	99.28; Pred. No. 2.9e-85;
Matches	Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	9 KKVFFVLYTFLGLTISQEVFAQDPDPQLHRSSSLVKNLQNLVFLYEGDPVTYHENKSV 68
Db	1 KKVFFVLYTFLGLTISQEVFAQDPDPQLHRSSSLVKNLQNLVFLYEGDPVTYHENKSV 60
Qy	9 DQLLSDHLLYNNSPNYGPNNPDKLTKLQNEATLFDKNDVYIYGYYHICLCAENARSAC 128
Db	1 KKVFFVLYTFLGLTISQEVFAQDPDPQLHRSSSLVKNLQNLVFLYEGDPVTYHENKSV 61
Qy	129 IGGYTNHEGNHLEIPKPKLIVVYKSIDGIOSLSPDIETNKMKVTAQELDYKVRKYLTDNQK 188
Db	121 IGGYTNHEGNHLEIPKPKLIVVYKSIDGIOSLSPDIETNKMKVTAQELDYKVRKYLTDNQK 180
Qy	189 LYNGPSKVEGTGTFKIPKNKESWDFPPEPFTOSKYLMIYKDNETLDSNTSQI 244
Db	181 LYNGPSKVEGTGTFKIPKNKESWDFPPEPFTOSKYLMIYKDNETLDSNTSQI 236

C: Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
 C: Accession: S18789
 R: Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
 J. Exp. Med. 174, 1271-1274, 1991
 A: Title: Characterization and clonal distribution of four alleles of the speA gene
 A: Reference number: S18782; MUID:9204423; PMID:1940804
 A: Accession: S18789
 A: Status: nucleic acid sequence not shown; translation not shown
 A: Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C: Genetics:
 A: Gene: speA
 C: Superfamily: enterotoxin B
 C: Keywords: exotoxin
 F: 1-22/Domain: signal sequence (fragment) #status predicted <S>
 F: 23-236/Product: exotoxin A (fragment) #status predicted <NAT>
 Query Match 83.7%; Score 1108; DB 2; Length 236;
 Best Local Similarity 88.6%; Pred. No. 6.7e-76;
 Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0
 Qy 9 KKKMFVFLVFLGLISQEYFAQQDDPSQLHRSLLVKLNQNIYFLYEGDPVTHENKSV 6
 Db 1 KKIVYFVLFLGLTTSOQEYFAQQDENPSQLHRSLLVKLNQNIYFLYEGDPVTHENKSV 6
 Qy 69 DQLLSSHLLYVNSGPNYDQLKTELNQEMATLFDKRNVDIYGEYVHLCGNAERSAC 1
 Db 61 DQLLSSHLLYVNSGPNYDQLKTELNQEMATLFDKRNVDIYGEYVHLCGNAERSAC 1
 Qy 129 IGGYTINHEGNHLIETPKKIVVSKDGIOSLSFDIETSKKTAQELDYKVKYKLTDNKQ 1
 Db 121 IGGYTINHEGNHLIETPKNLLVSKDGIOSLSFDIETSKKTAQELDYKVKYKLTDNKQ 1
 Qy 189 LYTNPSKSYETGYKIFPKNKESENDFEPEFEFTOSKLYKMDNETLDSNTSQI 244
 Db 181 LYTNPSKSYETGYKIFKSKDKESENDFEPEFEFTOSKLYKMDNETLDSNTSQI 236

RESULT 5
 A26152 streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
 N: Alternative names: scarlet fever toxin; SPE type A (speA)
 C: Species: Streptococcus sp.
 C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C: Accession: A26152
 R: Johnson, L.P.; L'Italien, J.J.; Schlevert, P.M.
 Mol. Gen. Genet. 203, 354-356, 1986
 A: Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to streptococcal pyrogenic exotoxin type B
 A: Reference number: A26152; MUID:86284313; PMID:3526093
 A: Accession: A26152
 A: Molecule type: DNA
 A: Residues: 1-250 <JOH>
 C: Superfamily: enterotoxin B
 C: Keywords: exotoxin

Query Match 81.2%; Score 1074.5; DB 1; Length 250;
 Best Local Similarity 83.7%; Pred. No. 2.3e-73; Indels 1; Gaps 0
 Matches 210; Conservative 7; Mismatches 1; Indels 1; Gaps 0
 Qy 1 MENNNKVLKKMVFVFLVFLGLTISQEYFAQQDDPSQLHRSLLVKLNQNIYFLYEDPVL 6
 Db 1 MENNKEVKKMVFVFLMKEFLGTTPKGICSTRKPEQLNVLKTFKIVYFFMRYTTLV 6
 Qy 61 THENKYSVDQLLSHLDDIYNNSGPNYDQLKTELNQEMATLFDKRNVDIYGEYVHLCYC 1
 Db 61 THENKYSVDQLLSHLDDIYNNSGPNYDQLKTELNQEMATLFDKRNVDIYGEYVHLCYC 1
 Qy 121 ENAERSACIYGGTINHEGNHLIETPKKIVVSKDGIOSLSFDIETSKKTAQELDYKVR 1
 Db 121 ENAERSACIYGGTINHEGNHLIETPKKIVVSKDGIOSLSFDIETSKKTAQELDYKVR 1
 121 ENAERSACIYGGTINHEGNHLIETPKKIVVSKDGIOSLSFDIETSKKTAQELDYKVR 1

Qy 181 KYLTDNKQLYNTGSKYETGYIKEIPKNEFWDEFFPEPEFTQSKYLMYKDNELDSN 240
 Db 180 KYLTDNKQLYNTGSKYETGYIKEIPKNEFWDEFFPEPEFTQSKYLMYKDNELDSN 239

Qy 241 TSQIEVLTIK 251
 Db 240 TSQIEVLTIK 250

RESULT 6
 ENSA86
 enterotoxin B precursor - *Staphylococcus aureus*
 C;Species: *Staphylococcus aureus*
 C;Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
 C;Accession: S7360; A92065; S2740; A01815
 R; Jones, C.L.; Khan, S.A.
 J; Bacteriol. 166: 29-33, 1986
 A;Title: Nucleotide sequence of the enterotoxin B gene from *Staphylococcus aureus*.
 A;Reference number: S27360; MUID:86168029; PMID:39578099
 A;Accession: S7360
 A;Molecule type: DNA
 A;Residues: 1-366 <D0N>
 A;Cross-references: EMBL: M11118; NID: g152999; PIDN: AAA88550.1; PID: g153000
 A;Experimental source: strain S6
 R; Huang, I.Y.; Bergdoll, M.S.
 J; Biol. Chem. 245: 3518-3525, 1970
 A;Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide:protein
 A;Accession: A92065
 A;Molecule type: protein
 A;Residues: 28-55, NND-59-68, 'NE', 71, 'FDLIVL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',
 A;Experimental source: strain S-6
 R; Huang, I.Y.; Bergdoll, M.S.
 J; Biol. Chem. 245: 3511-3511, 1970
 A;Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition
 A;Reference number: A92064; MUID: 71007901; PMID: 54708221
 A;Contents: annotation; tryptic peptides
 R; Schmitz, E.J.; Roessner, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
 J; Biol. Chem. 245: 3493-3510, 1970
 A;Title: Purification of staphylococcal enterotoxin B.
 A;Reference number: A90548; MUID: 66035192; PMID: 495312
 A;Contents: annotation; biological source of protein
 R; Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Mostakaleva, E.Y.; Sveshnikov, J.; Biochem. 209, 833-828, 1993
 A;Title: Identification of functionally active fragments of staphylococcal enterotoxin B.
 A;Reference number: S27240; MUID: 93049338; PMID: 1425690
 A;Molecule type: protein
 A;Residues: 28-42:128-148 <ALA>
 C;Superfamily:
 C;Keywords: enterotoxin; extracellular protein; toxin
 F; 1-27/Domain; signal sequence #status predicted <SIC>
 F; 18-266/Product: enterotoxin B #status experimental
 F; 120-140/Disulfide bonds: #status experimental

Query Match 43.5%; Score 575.5; DB 1; Length 266;
 Best Local Similarity 48.2%; Pred. No. 6.2e-36; Indels 19; Gaps 7;

Matches 123; Conservative 38; Mismatches 75; Molecule type: DNA
 A;Residues: 1-266 <BOH>
 A;Accession: B60114
 A;Molecule type: protein
 A;Residues: 28-66 <BOH2>
 R; Couch, J.L.; Betley, M.J.

Db 131 SHQTDKTKTQSKYLMYKDNELDSN 251
 Qy 179 VRKYLTDNKQLYNTGSKYETGYIKEIPKNEFWDEFFPEP - EFTQSKYLMYKDN
 Db 191 TRHLYVKKLYEFNNSPQYEGYIKFT - ENENFSWYDMMPAGDKFDQSKYLMYND
 Qy 237 LDSNTSQIEVLTIK 251
 Db 250 VDSKDVYKIEVLTIK 264

RESULT 7
 S11885
 enterotoxin C3 - *Staphylococcus aureus*
 C;Species: *Staphylococcus aureus*
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1997
 C;Accession: S11885
 R; Horvde, C.J.; Hackett, S.P.; Bohach, G.A.
 Mol. Gen. Genet. 220: 329-333, 1990
 A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 A;Reference number: S11885; MUID: 90220508; PMID: 2135627
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-266 <HOV>
 A;Cross-references: GB:X51661; NID: 946570; PIDN: CAA335972.1; PID: 946571
 C;Superfamily: enterotoxin B
 Query Match 41.6%; Score 550.5; DB 2; Length 266;
 Best Local Similarity 46.1%; Pred. No. 4.7e-34; Indels 17; Gaps 17; Mismatches 74; Molecule type: DNA
 Matches 117; Conservative 46; Indels 17; Gaps 17; Mismatches 74
 Qy 15 VLTYEFLGLTIS-QEYFAQQDPD -PSQLHRS -LYVNLQNYFYLEGDPYHCVYHLCYC - EN
 Db 11 ILIFALILVLTSPVLAESQDPMPDDLHSSEEFGTGMGNKYLDDHHSYATVKYS
 Qy 71 LLSSHLLIYNNVSG -- PNYDKLKTTELKQNEMATLFKDKNVDIYGVYHLCYC - EN
 Db 71 FLAHLIYNTISDKKKLKNYDKVKTTELNEFLAKKYZDEVVYGSNYYVNCYFSSKDN
 Qy 126 ---SACIYGVTNHEGNHLEIP - KKVIVVKSTIDGIQSLSFIDTNNKRVTAQELD
 Db 131 VTGGRTCMYGGITKHEGNHDGNGNLQVNVYENKRNTISFEQVTDKSKVTAQELD
 Qy 180 RYKYLTDNKQLYNTGSKYETGYIKEIPKNEFWDEFFPEP - EFTQSKYLMYKDN
 Db 191 RNFLNKKLYEFNNSPQYEGYIKFT - ENENFSWYDMMPAGDKFDQSKYLMYND
 A;Title: Identification of functionally active fragments of staphylococcal enterotoxin B
 A;Reference number: S27240
 A;Molecule type: protein
 A;Residues: 1-266 <BOH>
 A;Accession: B60114
 A;Molecule type: protein
 A;Residues: 28-66 <BOH2>
 R; Couch, J.L.; Betley, M.J.

RESULT 8
 A60114
 enterotoxin C-2 precursor - *Staphylococcus aureus*
 N;Alternative names: enterotoxin C-3 precursor.
 C;Species: *Staphylococcus aureus*
 C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1992
 C;Accession: A60114; B60114; A33866
 R; Bohach, G.A.; Schlievert, P.M.
 Infect. Immun. 57, 2249-2252, 1989
 A;Title: Conservation of the biologically active portions of staphylococcal enterotoxin C-2 precursor - *Staphylococcus aureus*
 A;Reference number: A60114; MUID: 89277549; PMID: 2543637
 A;Accession: A60114
 A;Molecule type: DNA
 A;Residues: 1-266 <BOH>
 A;Accession: B60114
 A;Molecule type: protein
 A;Residues: 28-66 <BOH2>
 R; Couch, J.L.; Betley, M.J.

Qy 15 VLTYEFLGLTIS-QEYFA - QDQDPDSQYHRSILVKNL-QNIVFLYEGDPYHCVYHLCYC
 Db 11 ILIFALILVLTSPVLAESQDPMPDDLHSSEEFGTGMGNKYLDDHHSYATVKYS
 Qy 71 LLSSHLLIYNNVSGP - NYDKLKTTELKQNEMATLFKDKNVDIYGVYHLCYC
 Db 71 FLYFDLISIKDITKLGNYDNVYEFKNDLADKDYKDVYDVSANYYYQCYFSKKTNDIN 130
 Qy 124 ---ERSACIYGVTNHEGNHLEIPKKTIVVSKMVTQAEQDYLK 178

J. Bacteriol. 171, 4507-4510, 1989
 A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
 A;Reference number: A33866; MUID:932174; PMID:247399

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-266 <C0U>
 A;Cross-references: GB:M28364; NID:9153003; PIDN:AAA26624.1; PID:g153004
 C;Genetics:
 A;Gene: entC2
 C;Superfamily: enterotoxin B
 F;1-7/Domain: signal sequence #status predicted <SIG>
 F;2-8-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match Score 548; DB 2; Length 266;
 Best Local Similarity 44.1%; Pred. No. 7.2e-34;
 Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;

11 MVF-FVLTFLGLTISQEVAQODPSOLHRSS-LVKNLQNTYFLYEGDPVHENVKSY 68
 12 LIFALLVLVLETPNVAE--SQPDPTPDELHKSSSEETGTMGNMXYLYDDHYSATKVMSSV 68

Db RESULT 10
 G99968
 extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: G99968
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
 ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1235-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311932; PMID:11418146
 A;Accession: G99968
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-258 <RDR>
 A;Cross-references: GB:BA000018; PID:g13701617; PIDN:BA842910.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: seq
 C;Superfamily: enterotoxin B

Query Match Score 480; DB 2; Length 258;
 Best Local Similarity 40.7%; Pred. No. 8.6e-29; Mismatches 91; Indels 16; Gaps 5;
 Matches 105; Conservative 46; Mismatches 91; Indels 16; Gaps 5;

Db QY 8 LKMKMFFVLYTFLGLTISQEVAQODPDP - SOLHRSSLYKN---LQNITYFLYEGDPVT 61
 1 MKLSTVIIIIILTEVFNHNNNNVNAQDPDKLDELNKRSVDYNNKGTMGNVANLYTSPPV 60

Db QY 62 HENVKSYVDQLLSSHHLYNNVSGPNYDKLKTKEQNQENATLFKDNVYDLYGVEYHLCYLC 121

Db QY 61 GRGVINSRQFLSHDLIPIEKEYSYNEVKTTELNTLANNYDKKKVDFGVPYFYTCIPK 120

Db QY 122 NAE--- - RSCAYGVTNHNLBPIKTKVSYDGTQISLSPDIETKMVTAQEL 175

Db QY 121 SEPDINQNFGGCCMGGLTINSEN ERDKLITVQYTDNRQSLGFTITNNKNAVITQEL 179

Db QY 176 DYKVRKYLTDNQKQLQVLTNGPSKVTGTYKTFIPKNESEWDFPPEPE---FRTQSKYLMYK 232

Db QY 180 DYKARHWLTKERKLYERDGSAFESGKTFKPFYKFLNIYQ 239

Db QY 233 DNETLDSNTSQIEVLT 250

Db QY 240 DNKVVDSKSKTRMEVFLNT 257

RESULT 11
 A33953
 enterotoxin D Precursor - Staphylococcus aureus
 C;Species: Staphylococcus aureus
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
 C;Accession: A33953

Query Match Score 547; DB 14; Length 266;
 Best Local Similarity 44.5%; Pred. No. 8.6e-34;
 Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;

11 MVF-FVLTFLGLTISQEVAQODPSOLHRSSLYKNL-QNITYFLYEGDPVTHENVKSY 68

R; Bayles, K.W.; Iandolo, J.J. J. Bacteriol. 171, 4799-4806, 1989	A; Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin A; Reference number: A33953; MUID: 89359112; PMID: 2549000
A; Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-258 <BAY>	
A; Cross-references: GB:M28521; NID:91492109; PIDN:AAB06195.1; PMID:9758691	
C; Superfamily: enterotoxin B	
Query Match 26.1%; Score 345; DB 2; Length 258;	
Best Local Similarity 35.6%; Pred. No. 1.1e-18;	
Matches 93; Conservative 47; Mismatches 101; Indels 20; Gaps 10;	
Qy 8 LKKM-VFFVLYTFLGTTISO-EVFAQODPD---PSOLHR-----SSLYKLNQNLQIYFLYEG 57	
Db 1 MKKFLNLLAFLFTSLVISPLRKVANIDTSKEKEIHKKSLSLSLSTALNNMKHSY--ADK 58	
Qy 58 DPVTHENVKSYVDQLLSHLLIYN--VSGPNYDQLKTELKNOEMATLFKDKNDVYIYGVEYY 114	
Db 59 NPIIGENKSPGDQFFLNTLYKKFTFLDNLINPFDLILINNSKEMAQHFKSKVNDVYPIRYS 118	
Qy 115 HLCYLCENAEATRSACIYGGVTVNHEGNNHLEIPKPKVYKSVSDQ-SLUSFD-TETNNKRMVTA 172	
Db 119 INCYGE-IDRTACTYGGVTPHEGKLKERKPKIPINLWINGVKEYSLDKVQTDKKRMVT 177	
Qy 173 QELDKVYKVRVLTDNQQLYTGTP--SKYETGYIKFKPKNKESEFWFDFPEPEFTQSKYLM 230	
Db 178 QELDPAQARRYLQDKLQKLYNNDTLGKIQRGKIEFFSSDGSKVSYDLFDVKGDFPPEQLRI 237	
Qy 231 YKDNTLDSNTSQIEVYLTIK 251.	
Db 238 YSDNKTLSFEHLHDIYLYEK 258	
RESULT 12	
C89984 enterotoxin P [Imported] - Staphylococcus aureus (strain N315)	
C; Species: Staphylococcus aureus	
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001	
C; Accession: C89984	
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani, A.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001	
A; Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.	
A; Reference number: A89758; MUID: 21311952; PMID: 11418146	
A; Accession: C89984	
A; Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-260 <KUR>	
A; Cross-references: GB:BA000018; PID:913701743; PIDN:BAB43036.1; GSPDB:GN00149	
C; Experimental source: strain N315	
C; Genetics:	
A; Gene: sep	
C; Superfamily: enterotoxin B	
Query Match 25.8%; Score 341; DB 2; Length 260;	
Best Local Similarity 34.5%; Pred. No. 2.3e-18;	
Matches 92; Conservative 52; Mismatches 85; Indels 38; Gaps 13;	
Qy 10 KMVFVFLYTFGLITI-----SQEVAQDQDPDPSQHLRSSLVKNLQNLQIYFLYEGD 58	
Db 5 KRTTFPLSFLATLTSPLSPFVNCSESEEINGKDLQKKSLEQGTL-SNLRCOTYY-HNGS 62	
Qy 59 PVTTHENVKSYVDQLLSHLLIYN--VSGPN-YDKLKTFLKNOEMATLFKDKNDVYIYGVEYY 115	
Db 63 AII-ENKESDQFLAKTILFDFFGTCHOWNDLVLQGSKDNTANTIKGKVKDLYGYY-- 119	
Qy 116 LCYLCENAE--RSACTYGGVTVNHEGNNHLEIPKPKVYKVSIDGIQL--SFQJETNNKRMV 171	
Db 120 -GYQCTGTFPKTACMYGGVTLHDNNQLEEEKKVTPGLTVKTNKEVT 178	

Qy 1 MENNKVULKMMVFFVLYTFLGLTISQEYVFA-QQDPDPSQLHRSSLYK--NLQNIYFLYEG 57
 Db 1 MKNSKVMN--VLLILNLIACTCSVNNAYANEEPDKEFSLCKKSSVDPIALHNINDYIN 58
 Qy 58 DPVTHENYKV ---DQLLSHHLIYN ---VSG--PNYDKLKTTELKNQEMATLFKDKNVDI 107
 Db 59 NRFT--TVKSVTSTTEKFDFDLFKSINWLDGISAEEFKDLKVEFSSSAISKEFLGKTVD 116
 Qy 108 YGVEYYHLCLCENAEARSACIYGGTNTNHEGNHLEPKIVKVKSFDGIQSLSFDIETNK 167
 Db 117 YGYYKAHCH-GERQVDTACTYGGTPHENKKLSEPKNIGAVYDKNVNNTFIVTIDK 175
 Qy 168 KMVTAQELDYKVRKYLTDNKOLYTNGPSKYENGYIKP--IPKPKESFWDFPPEPFTQS 225
 Db 176 KVKTAQELDIKVRTKLNAYKLYDRNTSDVQKGYIKPFSHSEHKESEFYDLYIKSNLPD 235
 Qy 226 KYLMYKDNETLDSNTSNTSQIEVLT 250
 Db 236 QYIQQYNDNKTIDSSYHIDVLF 260

RESULT 15

H89968
 enterotoxin Sen [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus*
 C;Date: 10-May-2001 #sequence,revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: H89968
 R;Kuroda, M.; Ohta, T.; Uchiyana, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: H89968
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-258 <KUR>
 A;Cross-references: GB:BA000018; PID:913701618; PIDN:BAB42911.1; GSPDB:GN00149

C;Experimental source: strain N315
 C;Genetics:
 A;Gene: sen
 C;Superfamily: enterotoxin B
 Query Match 23.9%; Score 316.5; DB 2; Length 258;
 Best Local Similarity 34.2%; Pred. No. 1.5e-16;
 Matches 90; Conservative 49; Mismatches 101; Indels 23; Gaps 10;
 C;Accession: H89968
 Qy 1 MENNKVULKMMVFF--VLYTFLGLTISQEYVFAQOD---PPDSQLHRSSLYKLNQNY-- 52
 Db 1 MKNIKIKLMR--LFIYAAIITLCLINNNYNAEVKDLKKSDDSSKLF-NLTSYYT 57
 Qy 53 -FLYEGDPVTHENVKSVDQLLSHHLI---YNYSGPNYDQLKTELKNQEMATLFKDKNVDI 108
 Db 58 DITWQOLD---EENKISPDQNLNTTLLKNIDISVLTSSLKVEEFNSSDLANQFKGKNDI 114
 Qy 109 YGVEYYHLCY-LCNAEARSACIYGGTNTNHEGNHLEPKIVKVKSFDGIQSLSFDIETNK 167
 Db 115 YGLYFGNCKVGGLTE--EKTISCLYGGVTHDGNOLDEEKVIGVNFDGVQEGFVTKKK 172
 Qy 168 KMVTAQELDYKVRKYLTDNKOLYTNGPSKYENGYIKPKN--KESEFWDFPPEPFTQS 225
 Db 173 AKVTVAQELDIKVRTKLNAYKLYDRNTSDVQKGYIKPFSHSEHKESEFYDLYIKSNLPD 232
 Qy 226 KYLMYKDNETLDSNTSNTSQIEVLT 248
 Db 233 EPPQFVSDNRTVYSSSYHIDVPL 255

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 21, 2003, 12:14:04 ; Search time 74 Seconds
(without alignments)
875.287 Million cell updates/sec

Title: US-09-308-830a-13
Perfect score: 1323
Sequence: 1 MENNNKKVLLKKWFFVLYTFL.....KDNETLDSNTSQIEVYLT K 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacterioplasm:*

17: sp_archaea:*

ALIGNMENTS

RESULT 1	Q8K6K5	PRELIMINARY;	PRT;	251 AA.
ID	Q8K6K5			
AC	Q8K6K5;			
DT	01-OCT-2002 (TREMBLref. 22, Created)			
DT	01-OCT-2002 (TREMBLref. 22, Last sequence update)			
DT	01-MAR-2003 (TREMBLref. 23, Last annotation update)			
DE	Exotoxin type A-phage associated.			
GN	SPEA3 OR SPYM3_1301.			
OS	Streptococcus pyogenes (serotype M3).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptocaceae;			
OC	Streptococcus; Streptococcus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MGSA315 / Serotype M3;			
RX	MEDLINE=22133808; PubMed=12122206;			
RA	Beres S.B., Sylvia G.L., Barbian K.D., Lei B., Hoff J.S.,			
RA	Mammarella N.D., Liu M.-Y., Smotro J.C., Porcella S.F., Parkins L.D.,			
RA	Campbell D.S., Smith T.M., McCormick J.R., Leung D.Y.M.,			
RA	Schlievert P.M., Musser J.M.;			
RT	"Genome sequence of serotype M3 strain of group A Streptococcus:			
RT	Phage-encoded toxins, the high-virulence phenotype, and clone			
RT	emergence."			
RL	PROTEIN; AE014161; AAC908.1; -.			
DR	EMBL; PR006177; Bctr1_tox.			
DR	InterPro; IPR006123; Staph/Strep_toxin.			
DR	InterPro; IPR006126; Staph/Strep_tox.			
DR	InterPro; IPR006173; Staph_tox_OB.			
DR	Pfam; PF01123; Staph/Strep_toxin; 1.			
DR	Pfam; PF02876; Staph/Strep_tox.C; 1.			
DR	PRINTS; PR00279; BACTRIPROXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 251 AA; 92960 MW; 05E782CD01BFC05 CRC64;			

Query Match

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1313	99.2	251	16	Q8K6K5		Q8K6K5 streptococc
2	1239	93.7	236	2	P97163		P97163 streptococc
3	1238	93.6	236	2	Q54779		Q54779 streptococc
4	1233	93.2	236	2	Q57453		Q57453 streptococc
5	1172	88.6	222	2	Q9R931		Q9R931 streptococc
6	1108	83.7	236	2	Q54696		Q54696 streptococc
7	1053	79.6	222	2	Q9S524		Q9S524 streptococc
8	1053	79.6	222	2	Q938P4		Q938P4 streptococc
9	554	41.9	271	2	Q9F0L6		Q9F0L6 streptococc
10	552	41.7	266	16	Q8NXP6		Q8NXP6 streptococc
11	550	41.6	239	2	Q53678		Q53678 streptococc
12	549	41.5	239	2	Q06532		Q06532 streptococc
13	548	41.4	239	2	Q06533		Q06533 streptococc
14	547	41.3	239	2	Q06531		Q06531 streptococc
15	547	41.3	239	2	Q06535		Q06535 streptococc
16	543	41.0	239	2			

Best Local Similarity	99.2%	Pred. No.	1.3e-85;
Matches	249;	Conservative	1;
		Mismatches	1;
		Indels	0;
		Gaps	0;
QY	1	MENKKVKKMVFVFLGLTISQEVFAQDPDPSQLHRSVLYKLNQNYFLYEGDPVTHENYKSV	68
Db	1	MENKKVKKMVFVFLGLTISQEVFAQDPDPSQLHRSVLYKLNQNYFLYEGDPVTHENYKSV	60
QY	61	THENYKSYDQLLSHLIVNVSGPNYDALKTELKNQENATLFKDKNVTDYGVEXYHLCYLC	120
Db	61	THENYKSYDQLLSHLIVNVSGPNYDALKTELKNQENATLFKDKNVTDYGVEXYHLCYLC	120
QY	121	ENERSACIYGGTNTKVVKSLSIDGIOSLSETEINNKMTAQELDYKVR	180
Db	121	ENERSACIYGGTNTKVVKSLSIDGIOSLSETEINNKMTAQELDYKVR	180
QY	181	KYLTDNKOLYTNPSPKTYKFKIPRNKESTWFDFPEPEFTQSKYLMYKDNETLDSN	240
Db	181	KYLTDNKOLYTNPSPKTYKFKIPRNKESTWFDFPEPEFTQSKYLMYKDNETLDSN	240
		RESULT	3
		Q54779	PRELIMINARY; PRT; 236 AA.
		ID	Q54779
		AC	Q54779; Q54613; Q54740; Q54741;
		DT	01-NOV-1996 (TREMBLrel. 01; Created)
		DT	01-NOV-1996 (TREMBLrel. 01; Last sequence update)
		DE	01-MAR-2003 (TREMBLrel. 23; Last annotation update)
		GN	DE Type A exotoxin precursor (Fragment).
		SPBA	GN
		OS	Streptococcus pyogenes.
		OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
		OC	Streptococcus
		OX	NCBI_TaxID:1314;
		RN	[1]
		RP	SEQUENCE FROM N.A.
		RC	STRAIN=MGAS24 AND MGAS158 AND MGAS485 AND MGAS491;
		RX	MEDLINE=92044323; PubMed=1940804;
		RA	Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
		RT	"Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes."
		RT	J. Exp. Med. 171:1271-1274 (1991).
		RL	DR EMBL: X61569; CAA43767.1; -
		DR	DR EMBL: X61572; CAA43770.1; -
		DR	DR EMBL: X61568; CAA43766.1; -
		DR	DR EMBL: X61570; CAA43768.1; -
		DR	DR EMBL: X61571; CAA43769.1; -
		DR	DR HSSP: P08035; 1B1Z; Bctr1 tox.
		DR	DR InterPro: IPR006177; Bctr1 tox.
		DR	DR InterPro: IPR006123; Staph/Strep_toxin.
		DR	DR InterPro: IPR006126; Staph/Strep_toxin.
		DR	DR InterPro: IPR006173; Staph_tox_OB.
		DR	DR Pfam: PF01123; Staph_Strep_toxin; 1.
		DR	DR Pfam: PF02876; Staph_STREP_TOX_C; 1.
		DR	DR PRINTS: PRO0279; BACTR1TOXIN.
		DR	DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
		DR	DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
		KW	Signal.
		FT	NON_TER 1 1
		FT	SIGNAL <1 22
		FT	CHAIN 23 >26
		FT	NON_TER 236 236
		SQ	SEQUENCE 236 AA; 27454 MW; 29DFZAD575623R4 CRC64;
		Query	Match 93.6%; Score 1238; DB 2; Length 236;
		Best Local Similarity	99.2%; Pred. No. 2.5e-80; Indels 0; Gaps 0;
		Matches	Conservative 1; Mismatches 1;
		FT	Local Similarity 99.2%; Pred. No. 2.5e-80; Indels 0; Gaps 0;
		FT	CHAIN 23 >26
		FT	NON_TER 236 236
		FT	SEQUENCE 236 AA; 27468 MW;
		QY	9 KKMVFVFLVTFGLTISQEVFAQDPDPSQLHRSVLYKLNQNYFLYEGDPVTHENYKSV
		Db	69 DOLLSHLLIYVNSGPYDALKTELKNQENATLFKDKNVTDYGVEXYHLCYLC
		QY	69 DOLLSHLLIYVNSGPYDALKTELKNQENATLFKDKNVTDYGVEXYHLCYLC
		Db	61 DOLLSHLLIYVNSGPYDALKTELKNQENATLFKDKNVTDYGVEXYHLCYLC

129	IGGYTNHGNHLETPKIVVKSIDGIGSLSFDETFNKKMVTQELDYKVRKYLTDNKQ	188	Db	181 LYNGPSKTYETGYIKFKPNKESWDFEFFPEPEFTOSKYLMIKYKDNELTDSNTSQI	236
121	IGGYTNHGNHLETPKIVVKSIDGIGSLSFDETFNKKMVTQELDYKVRKYLTDNKQ	180			
		RESULT 5			
	Q57453; PRELIMINARY; PRT; 236 AA.	Q9R931; PRELIMINARY; PRT; 222 AA.			
	Q57453; 01-NOV-1996 (TREMBLrel. 01, Created) 01-NOV-1996 (TREMBLrel. 01, Last sequence update) 01-MAR-2003 (TREMBLrel. 23, Last annotation update) Type A exotoxin precursor (Fragment).	Q9R931; 01-MAY-2000 (TREMBLrel. 13, Created) 01-MAY-2000 (TREMBLrel. 13, Last sequence update) 01-MAR-2003 (TREMBLrel. 23, Last annotation update) DE Exotoxin A (Fragment).			
	SPRA.	GN			
	Streptococcus pyogenes.	OS			
	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	OC			
	Streptococcus	OC			
	Streptococcus pyogenes.	OC			
	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	NCBI_TAXID=1314;			
	(1)	RN [1]			
	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.			
	STRAIN=AG9596;	STRAIN=D09;			
	MEDLINE=92044323; PubMed=1940804;	DR			
	Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;	DR			
	"Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes."	DR			
	J. Exp. Med. 174:1271-1274 (1991).	DR			
	EMBL: X61562; CAA43760; 1;	DR			
	EMBL: X61563; CAA3761; 1;	DR			
	EMBL: X61567; CAA3765; 1;	DR			
	EMBL: X61561; CAA43759; 1;	DR			
	EMBL: X61564; CAA3762; 1;	DR			
	EMBL: X61565; CAA3763; 1;	DR			
	EMBL: X61566; CAA43764; 1;	DR			
	HSSP: P08095; 1B12.	DR			
	InterPro; IP006177; Staph/Strep_toxin.	InterPro; IP006123; Staph/Strep_toxin.			
	InterPro; IP006116; Staph/Strep_toxin.	InterPro; IP006167; Staph_tox_OB.			
	InterPro; IP006173; Staph_tox_OB.	Pfam; PF01123; Staph_STREP_toxin; 1.			
	Pfam; PF02876; Staph_STREP_tox_C; 1.	Pfam; PF02876; Staph_STREP_tox_C; 1.			
	PRINTS; PS00279; BACTRUTOXIN.	PRINTS; PS00279; BACTRUTOXIN.			
	PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1.	PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1.			
	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
	NON_TER 1 1	NON_TER 1 1			
	SIGNAL <1 22	SIGNAL <1 22			
	CHAIN 23 >236	CHAIN 23 >236			
	NON_TER 236 236	NON_TER 236 236			
	SEQUENCE 236 AA: 27484 MW: 2EPT7F4AACB53600 CRC64;	SEQUENCE 236 AA: 27484 MW: 2EPT7F4AACB53600 CRC64;			
	POTENTIAL.	POTENTIAL.			
	TYPE A EXOTOXIN.	TYPE A EXOTOXIN.			
	Query Match 93.2%; Score 1233; DB 2; Length 236;	Query Match 93.2%; Score 1233; DB 2; Length 236;			
	Best Local Similarity 99.2%; Pred. No. 5.6e-80;	Best Local Similarity 99.2%; Pred. No. 5.6e-80;			
	Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
	DB	DB			
	RESULT 6	RESULT 6			
	Q54696; PRELIMINARY; PRT; 236 AA.	Q54696; PRELIMINARY; PRT; 236 AA.			
	AC Q54696;	AC Q54696;			
	DT 01-NOV-1996 (TREMBLrel. 01, Created)	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
	DE Type A exotoxin precursor (Fragment).	DE Type A exotoxin precursor (Fragment).			
	GN SPRA.	GN SPRA.			
	OS Streptococcus pyogenes.	OS Streptococcus pyogenes.			
	OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae.	OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae.			

Streptococcus												
OX	RN	SEQUENCE FROM N.A.										
RP	SEQUENCE FROM N.A.											
RC	STRAIN=MGAS156;											
RX	MEDLINE=92044323; PubMed=1940804;											
RA	Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;											
RT	"Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in											
RT	Streptococcus pyogenes."											
RT	J. Exp. Med. 174:1271-1274 (1991).											
RL	DR EMBL: X61573; CAR43771.1;											
DR	HSSP: P08095; 1B1Z;											
DR	InterPro: IPR006177: Bctrl_tox.											
DR	InterPro: IPR006123: Staph/Strep_toxin;											
DR	InterPro: IPR006126: Staph/Strep_tox.											
DR	InterPro: IPR006173: Staph_tox_OB.											
PFAM	PF01123; Staph_toxin_1.											
PFAM	PF02876; Staph_Surp_tox_C; 1.											
PRINTS	PR00279: BACTRTOXIN.											
PROSITE	PS00077; STAPH_STREP_TOXIN_1; 1.											
PROSITE	PS00278; STAPH_STREP_TOXIN_2; 1.											
KW	Signal											
FT	NON-TER	1	1									
FT	NON-TER	<1	22	POENTIAL.								
FT	CHAIN	23	>236	TYPE A EXOTOXIN.								
FT	NON-TER	236	236	236 AA; 236 AA;								
SQ	SEQUENCE											
Qy	9 KRMVVFVLYTFLGTLTISQEVFAQODPDSQLHRSSLVRLNQNITYFLYEGDPYTHEVNKSV	68										
Db	1 KKVIVFVIAFLGFLTTSDEVFAQDPDNFSQLHRSSLVRLNQNITYFLYEGDPYTHEVNKSV	60										
Qy	209 Best Local Similarity 88.6%; Matches 209; Conservative 14; Score 1108; Pred. No. 4.1e-71;	Length 236; Mismatches 13; Indels 0; Gaps 0;										
Db	61 DQLSHLJYNNSGLYNDKLTKELTKRNEMATLEFKDNVYDLYGVEYVHLCYLCENERSAC	128										
Qy	61 DQLSHLJYNNSGLYNDKLTKELTKRNEMATLEFKDNVYDLYGVEYVHLCYLCENERSAC	120										
Db	129 IYGGTNTHEGNHLEIPKAKVVKSIDGQSLSPDIETNKVKVTAQELDYKVRKHLTDNQ	188										
Qy	121 IYGGTNTHEGNHLEIPKAKVVKSIDGQSLSPDIETNKVKVTAQELDYKVRKHLTDNQ	180										
Db	189 LYTNPGSKYETGYKTFIPKRNKESFWDFPEPEFTQSRYLMITYKDNETLDSNTSQI	244										
Qy	181 LYTNPGSKYETGYKTFIPKRNKESFWDFPEPEFTQSRYLMITYKDNETLDSNTSQI	236										
Db	181 LYTNPGSKYETGYKTFIPKRNKESFWDFPEPEFTQSRYLMITYKDNETLDSNTSQI	236										
RESULT 7												
Q9S5Z4	ID Q9S5Z4	PRELIMINARY;	PRT;	222 AA.								
AC	Q9S5Z4;											
DT	01-MAY-2000 (TREMBLrel.	13, Created)										
DT	01-MAY-2000 (TREMBLrel.	13, Last sequence update)										
DT	01-MAY-2003 (TREMBLrel.	23, Last annotation update)										
DE	Exotoxin type A (Fragment).											
GN	SPEA											
OS	Streptococcus pyogenes.											
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;											
OC	Streptococcus.											
OX	NCBI_TaxID=1314;											
RP	SEQUENCE FROM N.A.											
RC	STRAIN=D633;											
RX	MEDLINE=99137798; PubMed=9952369;											
RA	Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M., Hollingshead S.K., Basil B.;											
RA	"Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci";											
RT	J. Infect Dis. 170:627-636 (1999);											
RT	DR ENBML: AF029051; AAD2115.1;											

RESULT 10						
QBNXJJ6	PRELIMINARY;	PRT;	266	AA.		
AC QBNXJJ6						
ID QBNXJJ6						
AC QBNXJJ6	PRELIMINARY;	PRT;	266	AA.		
DT 01-OCT-2002	(TREMBLrel. 22, Created)					
DT 01-OCT-2002	(TREMBLrel. 22, Last sequence update)					
DT 01-MAR-2003	(TREMBLrel. 23, Last annotation update)					
DE ENTEROTOXIN TYPE C PRECURSOR						
GN SEC4 OR MW0759.						
OS <i>Staphylococcus aureus</i> (strain MW2).						
OC Bacteria; Firmicutes; Bacillales; <i>Staphylococcus</i> .						
NCBI_TaxID=166620;						
[1]						
RN						
RP SEQUENCE FROM N.A.						
RX MEDLINE=22040717; PubMed=12044378;						
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu S.;						
RA "Genome and virulence determinants of high virulence community-acquired MRSA.";						
RT Lancet 359:1819-1827(2002).						
DR EMBL; AP004824; BAB94624.1; -.						
DR InterPro; IPR006126; Bcrl1_tox.						
DR InterPro; IPR006123; Strep/Strep_toxin.						
DR InterPro; IPR006173; Staph/Strep_tox.						
DR Pfam; PF01123; Staph_strep_tox_OB.						
DR Pfam; PF0076; Staph_strep_tox_C; 1.						
DR PRINTS; PR00279; BACTRUTOXIN.						
DR PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.						
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.						
KW Complete proteome.						
SQ SEQUENCE 266 AA; 30670 MW 4C654659AA48120F CRC64;						
Query Match 41.7%; Score 552; DB 16; Length 266;						
Best Local Similarity 44.5%; Pred. No. 1, 3e-31; Gaps 18; Gaps 114; Conservative 51; Mismatches 73; Indels 18;						
Matches 11						
QY 11 MVF-FVLYPFLGLTISQEVAFAQQDPPSQRHRS- LVKLNQNITYFEGDPVTHENVKSY						
Db 12 LIFALILVLFPTVNLAE--S-QDPDPDPELHKSSSEFTGNGNKMVLYYDDVSVATKVKS						
QY 69 DQLLSSHLLTVNSG--PNDTDLKPLKELKNQEMATLFLKDKVADYIYGVEYYHICYL--ENF						
Db 69 DKFLAHDLINVNISDKKLKNVDKVKTELLNEDLAKKYKDEVDVIGSNYYNYCYFSSKKDN						
QY 124 ER---SACYYGGTNHEGHNLHEIP--KKVVKVTSIDGQLSFDIETNKMTAQELD						
Db 129 GKVTCGKTCMGGTITKHEGHNFIDNGNLQNLYIRVNEKRNTISFEVQTDKSVTAQELD						
QY 178 KVRVLTNDKQLYTNGPSKVEGYIKFIPPKNESEWFDFPPEP--EFTQSKYLMYKDNT						
Db 189 KARFLINKKNNLYEFNNSSPPETGYKTFIENGNTFWYDMMAPGDKFQDSKLYMMYNDNN						
QY 236 TLDNTNTSQLEYYLTK 251.						
Db 249 TVDSRKV1BVHLTTK 264						
RESULT 11						
Q53678	PRELIMINARY;	PRT;	239	AA.		
ID Q53678						
AC Q53678;						
DT 01-NOV-1996	(TREMBLrel. 01, Created)					
DT 01-NOV-1996	(TREMBLrel. 01, Last sequence update)					
DT 01-MAR-2003	(TREMBLrel. 23, Last annotation update)					
DE Enterotoxin (Fragment).						
OS <i>Staphylococcus aureus</i> .						
OC Bacteria; Firmicutes; Bacillales; <i>Staphylococcus</i> .						
NCBI_TaxID=1280;						
[1]						

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CC	DISDSE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC FEVER.	FT	HELIX	224	227
CC	-1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.	FT	HELIX	228	231
CC	-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCAL TOXIN FAMILY.	FT	TURN	232	233
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions. There are no restrictions on its modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	FT	STRAND	236	238
CC	EMBL; U40453; AAC48668.1; -.	FT	TURN	239	241
CC	EMBL; X03929; CAA27568.1; -.	FT	STRAND	243	249
CC	DR; AE005982; AAL9141.1; -.	SEQUENCE	251 AA;	29246 MW;	54001FE4CCBCFC3 CRC64;
CC	DR; 1B1Z; 24-NOV-99.	Query Match	99.3%	Score 1314;	DB 1; Length 251;
CC	DR; 1FNU; 17-NOV-00.	Best Local Similarity	99.6%	Pred. No. 1-2e-92;	Indels 0; Mismatches 0;
CC	DR; 1FNV; 17-NOV-00.	Matches 250;	Conservative	1;	
CC	DR; 1FNW; 17-NOV-00.	QY	1 MENNKYLKKMVKYEFVLYTFLGLTTISQYFQAQDPDPSOLHRSVLLQNLQNYFLYEC		
CC	DR; 1HA5; 03-APR-02.	Db	1 MENNKYLKKMVKYEFVLYTFLGLTTISQYFQAQDPDPSOLHRSVLLQNLQNYFLYEC		
CC	DR; 1L0X; 03-APR-02.	QY	61 THEVNKSVDQQLLSHLILYNNSGSPNYPDKLTELKLNQEMATLFKDVKVNDIYGVYEHILC		
CC	DR; Bctr1; IPR006177; Bctr1_tox.	Db	61 THEVNKSVDQQLLSHLILYNNSGSPNYPDKLTELKLNQEMATLFKDVKVNDIYGVYEHILC		
CC	DR; InterPro; IPR006123; Staph/Strep_toxin.	QY	121 ENAERSACIYGEVTVNHHGNHLEIPKKVVKVSIDGIGLSFDIETNKKMVTAAQELDY		
CC	DR; InterPro; IPR006126; Staph/Strept_tox.	Db	121 ENAERSACIYGEVTVNHHGNHLEIPKKVVKVSIDGIGLSFDIETNKKMVTAAQELDY		
CC	DR; InterPro; IPR006173; Staph_tox_OB.	QY	181 KYLTDNQQLYNTGPKSKYETGYTKFIPKNEKSFWFDFPEPEFTQSKYLMYKDNENL		
CC	DR; Pfam; PRO0876; Staph/Strep_tox_C; 1.	Db	181 KYLTDNQQLYNTGPKSKYETGYTKFIPKNEKSFWFDFPEPEFTQSKYLMYKDNENL		
CC	DR; PRINTS; PF01123; Staph/Strep_toxin; 1.	QY	241 TSQIEVYLTTK 251		
CC	DR; PROSITE; PS00277; STAPH_STREP.	Db	241 TSQIEVYLTTK 251		
CC	DR; PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1.				
KW	Toxin; Signal; 3D-structure; Complete proteome.				
FT	SIGNAL	1	30	EXOTOXIN TYPE A.	RESULT 2
FT	CHAIN	31	251	EXOTOXIN TYPE A.	ETXB_STAAU
FT	DISULFID	117	128	K -> E (IN REF. 2).	ID
FT	CONFLICT	6	6	VT -> MK (IN REF. 2).	ETXB_STAAU
FT	CONFLICT	17	18	SQEVAQODD -> LPKGICSTRPK (IN REF. 2).	STANDARD
FT	CONFLICT	25	35	H -> Q (IN REF. 2).	AC
FT	CONFLICT	40	40	S -> N (IN REF. 2).	PO1552;
FT	CONFLICT	43	43	REF. 2).	DT
FT	CONFLICT	47	59	REF. 2).	13-AUG-1987 (Rel. 01, Created)
FT	CONFLICT	129	129	I -> L (IN REF. 2).	DT
FT	CONFLICT	165	178	TNKRMVTAQDLYK -> QIKNGNCRSIISYT (IN	15-SEP-2003 (Rel. 05, Last sequence update)
FT	HELIX	36	38	REF. 2).	DE
FT	HELIX	42	44	REF. 2).	Enterotoxin type B precursor (SEB).
FT	TURN	48	48	REF. 2).	GN
FT	HELIX	49	56	REF. 2).	OS
FT	STRAND	60	66	Staphylococcus aureus.	OC
FT	STRAND	69	69	Bacteria; Firmicutes; Bacillales; Staphylococcus.	NCBI_TaxID=1280;
FT	TURN	73	74	[1]	RN
FT	STRAND	75	78	SEQUENCE FROM N.A.	RN
FT	TURN	82	82	MEDLINE=86168029; PubMed=3957869;	RX
FT	TURN	83	84	Jones C.L., Khan S.A.;	RA
FT	STRAND	85	85	"Nucleotide sequence of the enterotoxin B gene from <i>Staphylococcus</i>	RT
FT	STRAND	87	91	<i>Escherichia coli</i> and <i>Staphylococcus aureus</i> .";	RT
FT	HELIX	95	101	Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854 (1985).	RL
FT	TURN	102	103	J. Bacteriol. 166:29-33 (1986).	RL
FT	STRAND	105	110	RN [2]	RN
FT	TURN	113	113	SEQUENCE OF 40-91 FROM N.A.	RN
FT	STRAND	115	116	MEDLINE=529855; PubMed=3898073;	RX
FT	STRAND	126	130	Raneelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;	RA
FT	STRAND	133	135	"Molecular cloning of staphylococcal enterotoxin B gene in	RT
FT	STRAND	137	138	<i>Escherichia coli</i> and <i>Staphylococcus aureus</i> .";	RT
FT	STRAND	140	153	J. Biol. Chem. 245:13518-13525 (1970).	RL
FT	TURN	154	155	RN [3]	RN
FT	STRAND	156	167	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).	RX
FT	STRAND	169	171	MEDLINE=9306291; PubMed=1436058;	RA
FT	HELIX	172	187	Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;	RT
FT	STRAND	199	205	"Crystal structure of staphylococcal enterotoxin B, a superantigen	RT
FT	STRAND	212	215	Nature 359:801-806 (1992).	RL

[5] X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RP MEDLINE-94203282; PubMed-8152483;
RX Jardetzky T.S.; Brown J.H.; Gorga J.C.; Stern L.J.; Urban R.G.,
RA Chi Y.I.; Stauffacher C.; Strominger J.L.; Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RT Nature 368:711-718(1994).
RL [6]
RN RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE-91096298; PubMed-9881971;
RA Li H.; Llera A.; Leder L.; Ysern X.; Schlievert P.M.,
RA Karjalainen K.; Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE-98181012; PubMed-9514739;
RA Papageorgiou A.C.; Tranter H.S.; Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
enterotoxin B at 1.5 Å resolution: implications for superantigen
recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: M11118; AAA88550_1; -.
DR PIR: S27360; ENSAB6.
DR PDB: 1SEB; 20-JUN-96.
DR 2SEB; 28-JAN-98.
DR 3SEB; 27-MAY-98.
DR 1SE3; 16-JUN-97.
DR 1SE4; 15-OCT-97.
DR 1SBB; 04-MAR-99.
DR 1DDM; 14-MAR-01.
DR 1DX; 28-JUN-00.
DR 1DSZ; 28-JUN-00.
DR 1D6S; 28-JUN-00.
DR InterPro: IPR006177; Bctrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00219; BACTRIL_TOXIN.
DR PROSITE: PS00077; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00078; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE B.
FT DISULFID 120 140
FT CONFLICT 56 58 DDN -> NND (IN REF. 3).
FT CONFLICT 69 77 DQFVYFDL -> NEFEDLVL (IN REF. 3).
FT CONFLICT 118 118 MISSING (IN REF. 3).
FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
FT CONFLICT 133 135 QTD -> ENT (IN REF. 3).
FT CONFLICT 149 150 NG (IN REF. 3).
FT CONFLICT 156 156 Y -> YY (IN REF. 3).
FT CONFLICT 185 186 QE -> EQ (IN REF. 3).
FT CONFLICT 233 233 D -> ND (IN REF. 3).
FT CONFLICT 246 247 DN -> ND (IN REF. 3).
FT CONFLICT 253 253

OS Staphylococcus aureus.
 OC Bacteria: Firmicutes; Bactillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M50 / ATCC 700659, and N315;
 RX MEDLINE=13111952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-T., Nagai Y., Lian J.-Q., Ito T.,
 RA Mizutani-Uji M., Matsukawa H., Maruyama A., Murakami H., Hosoya A.,
 RA Sekimizu K., Hirakawa H., Suhara S., Goto S., Yabuuchi J., Kaito C.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Hattori M., Yoshino C.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90220508; PubMed=2325627;
 RA Hovde C.J., Hackett S.P., Bohach G.A.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
 sequence comparison of all three type C staphylococcal
 enterotoxins.";
 RT Mol. Genet. 220:329-333(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=97064178; PubMed=8906397;
 RA Fields B.A., Malschgi E.L., Li H., Yseyn X., Stauffacher C.V.,
 RA Schlievert P.M., Karjalainen K., Mariuza R.A.;
 RT "Crystal structure of a T-cell receptor beta-chain complexed with a
 RT superantigen";
 RL Nature 384:188-192(1996).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC -1- STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 DR EMBL; APO03364; BAB58171.1; -.
 DR EMBL; APO03135; BAB4309.1; -.
 DR EMBL; X51661; CAA35972.1; -.
 DR PIR; S11885; S11885.
 DR PDB; 1JCK; 12-NOV-97.
 DR PDB; 1KUG; 02-AUG-02.
 DR PDB; 1KUJ; 14-AUG-02.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006133; Staph_tox_OB.
 DR Pfam; PF02876; Staph_Sirp_tox_C; 1.
 DR Pfam; PF01123; Staph_Sirp_toxin; 1.
 DR PRINTS; PRO0279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; signal; Superantigen; 3D-structure;
 KW Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
 FT DISULFID 120 137
 SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FFCA59 CRC64;
 Query Match 41.6% Score 550 5; DB 1; Length 266;
 Best Local Similarity 46.1%; Pred. No. 8.3e-35; Indels 17; Gaps 8;
 Matches 117; Conservative 46; Mismatches -74;

3 PDB: 1SB2; 08-MAR-96.	69 DKFLAHDLTINISDEKKLKNVDKVTKTELLNEDLAKYKDEVVYGGNNYVNCYFSSKDNV 128
3 PDB: 1COV; 19-SEP-01.	
3 PDB: 114P; 19-SEP-01.	
3 PDB: 114Q; 19-SEP-01.	
3 PDB: 114R; 19-SEP-01.	
3 PDB: 114X; 19-SEP-01.	
3 InterPro: IPR06127; <i>BctrL_tox.</i>	
3 InterPro: IPR06123; <i>Stap/Strep_toxin.</i>	
3 InterPro: IPR06126; <i>Staph/Strep_tox.</i>	
3 InterPro: IPR06173; <i>Staph_tox_OP.</i>	
3 InterPro: IPR06176; <i>Stap/Strep_tox_C; 1.</i>	
3 PRINTS; PR00279; <i>BACTRITOXIN.</i>	
3 PROSITE; PS00277; <i>STAPH_STREP_TOXIN_1;</i>	
3 PROSITE; PS00278; <i>STAPH_STREP_TOXIN_2;</i>	
3 Enteroxin; <i>Toxin; Signal; Superantigen; Metal binding; Zinc;</i>	
3 3D-structure.	
3 SIGNAL 1 27	RESULT 5
3 CHAIN 28 266 ENTEROTOXIN TYPE C-2.	ETC1_STAAU
3 DISULFID 120 137	ID ETC1_STAAU
3 METAL 36 36 ZINC.	STANDARD; AC P01553
3 METAL 110 110 ZINC.	PRT; 266 AA.
3 METAL 145 145 ZINC.	
3 METAL 149 149 ZINC.	
3 HELIX 35 37	DT 21-JUL-1986 (Rel. 01, Created)
3 HELIX 41 43	DT 01-JAN-1990 (Rel. 13, Last sequence update)
3 SPRAND 44 44	DT 28-FEB-2003 (Rel. 41, Last annotation update)
3 TURN 48 48	DE Enterotoxin type C-1 precursor (SEC1).
3 SPRAND 49 55	GN ENTC1.
3 SPRAND 60 65	OS <i>Staphylococcus aureus.</i>
3 STRAND 69 69	OC Bacteria; Firmicutes; Bacillales; <i>Staphylococcus.</i>
3 TURN 73 74	NCBI_TaxID=1280;
3 SPRAND 75 79	OX
3 TURN 83 86	RN [1]
3 STRAND 90 94	RP SEQUENCE FROM N.A.
3 HELIX 98 104	RX MEDLINE=8803852; PubMed=2823067;
3 TURN 105 106	RA Bohach G.A., Schlievert P.M.;
3 STRAND 109 113	RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
3 STRAND 116 116	RT relatedness to other pyrogenic toxins." ;
3 TURN 118 119	RL Mol. Gen. 209:15-20(1987).
3 TURN 128 129	RN [2]
3 SPRAND 136 139	RP SEQUENCE OF 28-266.
3 STRAND 142 144	RX MEDLINE=83213337; PubMed=6189824;
3 TURN 146 147	RA Schmidt J.J., Spero L.;
3 SPRAND 149 149	RT "The complete amino acid sequence of staphylococcal enterotoxin C1. ;
3 HELIX 151 153	RL J. Biol. Chem. 258:6300-6306(1983) .
3 STRAND 156 164	CC -1 SUBCELLULAR LOCATION: Secreted.
3 TURN 165 166	CC -1 DISEASE: STAPHYLOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
3 STRAND 167 176	CC STAPHYLOCCAL FOOD POISONING SYNDROME.
3 STRAND 178 178	CC -1 SIMILARITY: BELONGS TO THE STAPHYLOCCAL/STREPTOCOCAL TOXIN
3 STRAND 180 182	CC FAMILY.
3 HELIX 183 198	CC
3 STRAND 208 216	CC
3 TURN 218 219	CC
3 STRAND 222 226	CC
3 STRAND 232 232	CC
3 HELIX 237 241	CC
3 HELIX 242 246	CC
3 STRAND 249 251	CC
3 TURN 251 254	CC
3 STRAND 256 263	CC
3 SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;	CC
3 Query Match 41.4%; Score 548; DB 1; Length 266;	DR EMBL: X05615; OAA29260.1; -.
3 Best Local Similarity 44.1%; Pred. No. 1.3e-34;	DR PIR: S06356; ENSAC1.
3 Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;	DR HSSP: P34071; 1SE2.
3 SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;	DR InterPro: IPR06177; BctrL_tox.
3 Query Match 41.4%; Score 548; DB 1; Length 266;	DR InterPro: IPR06123; Staph/Strep_toxin.
3 Best Local Similarity 44.1%; Pred. No. 1.3e-34;	DR InterPro: IPR06126; Staph/Strep_tox.
3 Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;	DR InterPro: IPR06177; Staph/Strep_tox_OB.
3 SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;	DR Pfam: PF02876; Stap_Strep_tox_C; 1.
3 Query Match 41.4%; Score 548; DB 1; Length 266;	DR PRINTS: PR00277; BACTRITOXIN.
3 Best Local Similarity 44.1%; Pred. No. 1.3e-34;	DR PROSITE: PS00278; STAPH_STREP_TOXIN_1; 1.
3 Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;	DR Enterotoxin; Toxin; Signal; Superantigen.
3 SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;	FT SIGNAL 1 27 ENTEROTOXIN TYPE C-1.
3 Query Match 41.4%; Score 548; DB 1; Length 266;	FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
3 Best Local Similarity 44.1%; Pred. No. 1.3e-34;	FT DISUFD 120 137 D -> N (IN REF. 2).
3 Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;	FT CONFFLICT 177 177 SEQUENCE 266 AA; 30546 MW; 3A7AB59A98683B CRC64;
3 SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;	3Q DQLSHLILYINVSG---PYXDKLKLTELQEMATLFKDKNNDYVLYGVEYHLCYL--ENA 123

Query Match 41.3%; Score 547; DB 1; Length 266;
 Best Local Similarity 44.5%; Pred. No. 1.5e-34;
 Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;

Qy 11 MWF-FVLYTFLGLTISQEVPFAQDPDPQLRHSLLVKNL-ONIYFLYEGDPVTHENVKSV 68
 DR EMBL: AF064773; AAC266660.1; -;
 DR EMBL: AP003363; BAB57986.1; -;
 DR EMBL: AP003135; BAB2910.1; -;
 DR PIR: G89968; G89968.
 DR HSSP: P01552; 1SBB
 DR InterPro: IPR006177; Bctr1_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph/Strep_tox_C; 1.
 DR Pfam: PF01123; Staph/Strep_toxin_1; 1.
 DR PRINTS; PS00277; BACTR1OXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PROSITE; PS00278; Staph/Strep_toxin; Complete proteome.

Db 69 DFLFLDLYINSDKLLKNTDKVKTELLNECLAKKYKDEVVDVIGSNNYVNCYFSSKDNY 128
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph/Strep_tox_C; 1.
 DR Pfam: PF01123; Staph/Strep_toxin_1; 1.
 DR PRINTS; PS00277; BACTR1OXIN.

Qy 124 ER---SACIYGVTNHEGNLHEIP--KKIVVKVSTIDGIOSLSEDIETNKKMVTAQELDY 177
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PROSITE; PS00278; Staph/Strep_toxin; Complete proteome.

Db 129 GRTGGGTCTGMYGITHEGNFIDGNLQNVLYRVENKRNTISFEVQTDERSVPAQELDI 188
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph/Strep_tox_C; 1.
 DR Pfam: PF01123; Staph/Strep_toxin_1; 1.
 DR PRINTS; PS00277; BACTR1OXIN.

Qy 178 KVKYLTNDNKOLYTNGPSKTYETGYIKPIPNAKESTWDFDFFPEP- EFTQSKYLMYKDNE 235
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; Staph/Strep_toxin; Complete proteome.

Db 189 KARNEFLINKKNUYEFNSSPYETGYIKFIEENNNTFWYDMPAPGDKFQSKYLMYNDNK 248
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; Staph/Strep_toxin; Complete proteome.

Qy 236 TLDNTNSQIEVYLTTK 251
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; Staph/Strep_toxin; Complete proteome.

Db 249 TVDTSKSVKIEVHLTTK 264
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; Staph/Strep_toxin; Complete proteome.

RESULT 6

ETXG_STAAM

STANDARD; PRT; 258 AA.

AC 085382; PRT; 258 AA.

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Enterotoxin type G precursor (SEG).

GN ENTG OR SNG OR SAV1824 OR SA1642.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699),

OS Staphylococcus aureus (strain N315), and

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.

OX NCBI_Taxid=158878, 158879, 1280;

RN [1] RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=FR1572;

RX MEDLINE=98298056; PubMed=9632603;

RA Munson S. H., Tremaine M. T., Bettle M. J., Welch R. A.;

RT "Identification and characterization of staphylococcal enterotoxin

RT types G and I from staphylococcus aureus.";

RL Infect. Immun. 66:3337-3348(1998).

RN [2] RP SEQUENCE FROM N.A.

RC STRAIN=MU50 / ATCC 700699, and N315;

MEDLINE=21.311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Negai Y., Liyan J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mizutani U., Y. Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

RT aureus." Whole genome sequencing of meticillin-resistant Staphylococcus

RT aureus." Lancet 357:1225-1240(2001).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN

CC FAMILY.

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CC EMBL: AF064773; AAC266660.1; -;

CC EMBL: AP003363; BAB57986.1; -;

CC EMBL: AP003135; BAB2910.1; -;

CC PIR: G89968; G89968.

CC HSSP: P01552; 1SBB

CC InterPro: IPR006177; Bctr1_tox.

CC InterPro: IPR006123; Staph/Strep_toxin.

CC InterPro: IPR006126; Staph/Strep_tox.

CC InterPro: IPR006173; Staph_tox_OB.

CC Pfam: PF02876; Staph/Strep_tox_C; 1.

CC Pfam: PF01123; Staph/Strep_toxin_1; 1.

CC PRINTS; PS00277; BACTR1OXIN.

CC PROSITE; PS00278; STAPH_STREP_TOXIN_1; FALSE_NEG.

CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

CC PROSITE; PS00278; Staph/Strep_toxin; Complete proteome.

RT Zn²⁺-mediated homodimerization.";

RL EMBO J. 15:6812-6810(1996).

CC -|- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.

CC -|- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.

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CC

DR EMBL: M28521; AAB06195..1; -.

DR PIR: A33953; A33953.

DR HSSP: P13163; 1SXT.

DR InterPro: IPR006123; Staph/Strep_toxin.

DR InterPro: IPR006126; Staph/Strep_tox.

DR InterPro: IPR006173; Staph_tox_OB.

DR Pfam: PF01123; Staph/Strep_tox_C; 1.

DR Pfam: PF01123; Staph/Strep_toxin; 1.

DR PRINS: PR00275; BACTERIOTOXIN.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

KW Enterotoxin; Toxin; Signal; Superantigen; Zinc.

FT SIGNAL 1 25

FT CHAIN 26 258 ENTEROTOXIN TYPE D.

FT METAL 212 ZINC.

FT METAL 250 ZINC.

FT VARIANT 252 ZINC.

FT VARIANT 114 114 P -> A (IN STRAIN ATCC 2235).

SQ SEQUENCE 258 AA: 29746 MW; 4F7C6A28D42597FD CRC64;

Query Match 26.1%; Score 345; DB 1; Length 258;

Best Local Similarity 35.6%; Pred. No. 2.9e-19;

Matches 93; Conservative 47; Mismatches 101; Indels 20; Gaps 10;

Y 8 LKKM-VFFVLYFLGLITISQ-EVFAQDPD---PSQQLHR----SSLVKNLQNTYFLYEG 57

Db 1 MKKFNLIALLEFTSIVSPUNVKANEIDSVEKELHKKSELSSALANNMKHSY-ADK 58

Y 58 DPVTHENVKSDQQLSHLIVN--VSGPNYDKLTELKNQEMATFKDKNDVYGEVY 114

Db 59 NPIIGNKNSKGQFELNTLYKKFFDLINPFDLINFNSNEAQFKSKNVDYFIRYS 118

Y 115 HLCYLCENAERSACIIGGVINHEGNLIEPKKIVVSIDIQ-SLUSFD-TETNKKMVT 172

Db 119 INCYGE-IDRTACTGGVTHEGNKIPKIPILWINGVQKEVSLDKVQTDKKNVTV 177

Y 173 QELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFKPNKESFWFDEPEPEFTOSXYLMI 230

Db 178 QELDAQARRYQKDLYNNNDLGGIQRKGKIEFDSDGSKSYDIFDVKGDFPEQLR 237

Y 231 YKDNEFLDSNTSQIEVYLTIK 251

Db 238 YSDNKTLSTEHLHIDLYEK 258

RESULT 8

ETXE_STAAU STANDARD PRT: 257 AA.

ID ETEXE_STAAU

AC P12933;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Enterotoxin type E precursor (SEE).

GN ENTE.

OS *Staphylococcus aureus*.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

OX NCBI_TaxID:1280;

RN [11]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.

RC RN

RC P12933;

RX MEDLINE=88057005; PubMed=3384800;

RA Couch J.L., Soltis M.T., Befley M.J.;

RA "Cloning and nucleotide sequence of the type E *staphylococcal* enterotoxin gene.";

RT J. Bacteriol. 170:2954-2960(1998).

RL RN

RP 3D-STRUCTURE MODELING.

RX MEDLINE=96022987; PubMed=7552730;

RA Swaminathan S., Furey W.F. JR., Fletcher J., Sax M.;

RA "Residues defining V_beta specificity in *staphylococcal* enterotoxins.";

RT J. Bacteriol. 160:680-686(1985).

RL RN

RP 3D-STRUCTURE MODELING.

CC -|- COFACTOR: Binds 1. zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II (By similarity).

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

CC -|- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.

CC

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CC

DR EMBL: M21319; AAB26617..1; -.

DR PDB: 1SEE; A28179; DR

DR InterPro: IPR006173; Staph_tox_OB.

DR InterPro: IPR006123; Staph/Strep_tox.

DR InterPro: IPR006126; Staph_tox_C; 1.

DR Pfam: PF01123; Staph/Strep_toxin; 1.

DR PRINS: PR00275; BACTERIOTOXIN.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

DR InterPro: IPR006173; Staph_tox_OB.

DR InterPro: IPR006123; Staph/Strep_tox.

DR InterPro: IPR006126; Staph_tox_C; 1.

DR Pfam: PF01123; Staph/Strep_toxin; 1.

DR PRINTS: PRO0279; BACTERIOTOXIN.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

DR InterPro: IPR006173; Staph_tox_OB.

DR InterPro: IPR006123; Staph/Strep_tox.

DR InterPro: IPR006126; Staph_tox_C; 1.

DR Pfam: PF01123; Staph/Strep_toxin; 1.

DR PRINTS: PRO0279; BACTERIOTOXIN.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc.

KW

FT SIGNAL 1 27

FT CHAIN 28 257

FT METAL 211 211

FT METAL 249 249

FT METAL 251 251

FT METAL 33 35

FT HELIX 39 41

FT STRAND 42 42

FT TURN 46 47

FT HELIX 48 51

FT STRAND 52 54

FT HELIX 59 64

FT TURN 66 67

FT STRAND 69 69

FT TURN 73 74

FT STRAND 75 79

FT TURN 83 84

FT STRAND 90 94

FT HELIX 98 104

FT TURN 105 106

FT STRAND 109 113

FT STRAND 115 116

FT TURN 118 119

FT STRAND 128 132

FT STRAND 135 137

FT TURN 139 140

FT	STRAND	142	142	RN [3]
FT	STRAND	152	152	RP SEQUENCE OF 25-257; PubMed=3584106;
FT	STRAND	154	155	RX MEDLINE=8722229; PubMed=3584106;
FT	TURN	156	157	RA Huang I.-Y., Hughes J.L., Bergdol M.S., Schantz E.J.;
FT	STRAND	163	163	RR "Complete amino acid sequence of staphylococcal enterotoxin A.;"
FT	STRAND	171	171	RL Biol. Chem. 262:7006-7013(1987).
FT	STRAND	173	175	RN [4]
FT	HELIX	176	190	RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
FT	TURN	191	191	RX MEDLINE=9534648; PubMed=7628431;
FT	STRAND	203	211	RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohilstens M., Kalland T.,
FT	STRAND	219	221	RA Schlievert P.M., Ohlendorf D.R., Svensson L.A.;
FT	STRAND	227	227	RT "Crystal structure of the superantigen staphylococcal enterotoxin type A.";
FT	HELIX	234	239	RT RL EMBO J. 14:3292-3301(1995).
FT	STRAND	242	244	RN [5]
FT	TURN	245	247	RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
SQ	SEQUENCE	249	257	RX MEDLINE=97113025; PubMed=8943278;
SQ	SEQUENCE	257 AA;	29358 MW;	RA Sundstrom M., Hallen D., Svensson A., Dohilstens M.,
				RA Abrahamson L.;
				RT "The Co-crystal structure of staphylococcal enterotoxin type A with Zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.";
				RT RL J. Biol. Chem. 271:32212-32216(1996).
				RN [6]
				RP 3D-STRUCTURE MODELING.
				RX MEDLINE=96022987; PubMed=7552730;
				RA Swaminathan S., Pletcher J., Pletcher J., Sax M.;
				RT "Residues defining v beta specificity in staphylococcal enterotoxins.";
				RT RL Nat. Struct. Biol. 2:680-685(1995).
				RN [7]
				RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
				RX MEDLINE=9734375; PubMed=9191070;
				RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
				RT "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity."
				RT RL J. Mol. Biol. 269:270-280(1997).
				CC -1- COFACTOR: Bands 1 zinc ion per subunit. The zinc ion is necessary for the toxic interaction with MHC class II.
				CC -1- SUBUNIT: Monomer.
				CC -1- SUBCELLULAR LOCATION: Secreted.
				CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION SYNDROME.
				CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
				CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
				CC

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				CC
				DR EMBL; AP0428; BAB95754.1; -.
				DR PIR; M18970; AAA26681.1; -.
				DR PIR; A28664; A28664.
				DR PDB; 1ESP; 11-JUL-96.
				DR PDB; 1SXT; 19-NOV-97.
				DR PDB; 1D1Q; 21-FEB-02.
				DR PDB; 1IAG; 21-MAR-01.
				DR PDB; 1I4H; 21-MAR-01.
				DR InterPro; IPR006177; Bctr1_tox.
				DR InterPro; IPR006123; Staph/Strep_toxin.
				DR InterPro; IPR006126; Staph/Strep_toxin.
				DR InterPro; IPR006173; Staph_tox_OB.
				DR Pfam; PF02876; Staph_Strep_tox_C; 1.
				DR Pfam; PF01123; Staph_Strep_toxin; 1.
				DR PRINTS; PR00279; BACTRITOXIN.

PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; zinc; 3D-structure; Complete proteome.
 KW
 FT SIGNAL 1 24 ENTEROTOXIN TYPE A.
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISUFLID 25 130 ZINC.
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT METAL 242 242 T -> S (IN REF. 3).
 FT HELIX 28 31 HELIX
 FT TURN 32 33 TURN
 FT HELIX 39 41 HELIX
 FT TURN 44 45 TURN
 FT HELIX 46 55 HELIX
 FT TURN 56 56 TURN
 FT STRAND 59 65 STRAND
 FT TURN 73 74 TURN
 FT STRAND 75 78 STRAND
 FT TURN 79 80 TURN
 FT STRAND 90 94 STRAND
 FT HELIX 98 104 HELIX
 FT TURN 105 106 TURN
 FT STRAND 116 116 STRAND
 FT TURN 118 119 TURN
 FT STRAND 125 126 STRAND
 FT STRAND 128 132 STRAND
 FT STRAND 135 137 STRAND
 FT TURN 139 140 TURN
 FT STRAND 142 149 STRAND
 FT STRAND 151 155 STRAND
 FT TURN 156 157 TURN
 FT STRAND 158 160 STRAND
 FT HELIX 164 166 HELIX
 FT STRAND 167 171 STRAND
 FT STRAND 173 175 STRAND
 FT HELIX 176 191 HELIX
 FT TURN 193 194 TURN
 FT HELIX 197 199 HELIX
 FT TURN 200 200 TURN
 FT STRAND 205 212 STRAND
 FT STRAND 218 221 STRAND
 FT TURN 222 223 TURN
 FT HELIX 230 233 HELIX
 FT TURN 234 237 TURN
 FT STRAND 238 239 STRAND
 FT STRAND 242 244 STRAND
 FT STRAND 248 255 STRAND
 SQ SEQUENCE 257 AA: 29669 MW: ADEBF5BCA1F14677 CRC64: 7;
 Query Match 23 6%; Score 312; DB 1; Length 257;
 Best Local Similarity 31.3%; Pred. No. 9e-17; Mismatches 49; Conservative 81; Indels 22; Gaps 7;
 Matches 81; CC
 Qy 10 KMVFFYLTVLFFLGLTI-----SQEVPAQQDDPPSQLHRSSLYKVNQNLYFVYEGD 58
 Db 2 KKTAFFLFLFAITLTSPLYNGSERSEEINEKDLRKSELOQTAI-GNLKQIY-YYNE 58
 Qy 59 PVTHEVYKSYDOLSHLILY--VSGPNYDKLKTLEKNOEMATLFKDNVYDGYEYHH 115
 Db 59 KAKTENKESSHDFQFLQITLFFGFFTHSWYNDLIVDFDSKD1VDKVKGKVVDLYGAYGY 118
 Qy 116 LCYLCAENAEERSACIYGGVTHNHEGNHLEIPKIVKVSIDGIOSL-SFDIETNKKMVTQ 173
 Db 119 QC-AGGPNAKTCMGGVTLHDNNRTEKEKVPINFLWDGQNTVPELETVKINKMVTQ 177
 Qy 174 ELDYKVKYLIDNPKQLYTNG--PSKIVETGYIKFIPKANKESTWFDFPEPEFTQSKVLMY 231
 Db 178 ELDLQARRYLQEKNLYNNSDVFDKVQVRGLIVYHTSTEPSVNYDLEGAQGQYSNTLIRY 237
 Qy 232 KDNETLDSNTSQLEYVLT 250

Db 238 RDNKTTINSENNHHIDIVLYT 256
 RESULT 10
 SPEC_STRPY STANDARD PRT; 235 AA.
 ID SPEC_STRPY DT 01-JAN-1990 (Rel. 1.3, Created)
 AC P13380; DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
 RC STRAIN-T18P / MGAS 1585; DT 15-SEP-2003 (Rel. 4.0, Last annotation update)
 RX MEDLINE-88314303; PubMed-3045005;
 RA Goshorn S.C., Schliert P.M.;
 RT "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";
 RL Infect. Immun. 56:2518-2520(1988).
 RN [2]
 RN REVISIONS TO 21-26.
 RP STRAIN-T18P / MGAS 1585;
 RC NCBI_TAXID-1314;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
 RC STRAIN-T18P / MGAS 1585;
 RX MEDLINE-92363541; PubMed-1500157;
 RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RA Molecular population genetic evidence of horizontal spread of two
 RA alleles of the pyrogenic exotoxin C gene (spec) among pathogenic
 RA clones of Streptococcus pyogenes.";
 RL Infect. Immun. 60:3513-3517(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SF310 / ATCC 700294 / Serotype M1;
 RX MEDLINE-21192684; PubMed-11296296;
 RA Ferretti J.J., McShan W.M., Alidic D.J., Savic G., Lyon K.,
 RA Primeaux C., Serate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
 RA "Complete genome sequence of an M1 strain of Streptococcus
 RT Pyogenes";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
 RX MEDLINE-97397352; PubMed-9253413;
 RA Roussel A., Anderson B.F., Baker E.N., Baker E.N.;
 RT "Crystal structure of the streptococcal superantigen SPB-C:
 RT dimerization and zinc binding suggest a novel mode of interaction
 RT with MHC class II molecules.";
 RL Struct. Biol. 4:635-643 (1997).
 CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
 CC chain.
 CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC EXOTOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCCAL/STREPTOCOCAL TOXIN
 CC FAMILY.
 CC
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 DR EMBL; M3554; AAA27071; ALT_SEQ.
 DR EMBL; M97156; AAB59091; ALT_SEQ.
 DR

DR EMBL; M97157; AAB59092.1; . . .
 DR EMBL; AE006523; AAK33664.1; . . .
 DR PIR; A30509; A30509.
 DR PIR; A44799; A44799.
 DR PDB; 1ANB; 29-APR-98.
 DR PDB; 1KTK; 07-JUN-02.
 DR InterPro; IPR006127; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF0216; Staph_Strp_tox_C; 1.
 DR Pfam; PF01123; Staph_Strp_toxin; 1.
 DR PRINTS; PR00279; BACTERIOTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Toxin; Signal; 1
 KW Toxin; Signal; 3D-structure; Complete proteome; 27
 FT SIGNAL 1
 FT CONFLICT 53
 FT STRAND 33
 FT HELIX 44
 FT STRAND 49
 FT STRAND 59
 FT STRAND 63
 FT HELIX 67
 FT TURN 72
 FT STRAND 74
 FT STRAND 75
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 FT TURN 84
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 FT STRAND 92
 FT STRAND 93
 FT TURN 100
 FT TURN 109
 FT STRAND 110
 FT STRAND 114
 FT STRAND 117
 FT STRAND 119
 FT STRAND 127
 FT STRAND 128
 FT TURN 131
 FT TURN 135
 FT STRAND 136
 FT TURN 137
 FT STRAND 141
 FT TURN 142
 FT STRAND 144
 FT TURN 145
 FT STRAND 148
 FT STRAND 155
 FT HELIX 155
 FT TURN 156
 FT TURN 171
 FT STRAND 173
 FT TURN 174
 FT STRAND 176
 FT TURN 177
 FT STRAND 182
 FT TURN 189
 FT STRAND 190
 FT STRAND 194
 FT TURN 198
 FT STRAND 204
 FT HELIX 208
 FT HELIX 212
 FT STRAND 213
 FT TURN 217
 FT STRAND 220
 FT HELIX 222
 FT TURN 223
 FT STRAND 226
 FT STRAND 235
 Q0 SEQUENCE 235 AA; 27371 MW; 070534ABB952C1E0 CRC64;
 Q0 Best Local Similarity 16.2%; Score 214; DB 1; Length 235;
 Q0 Matches 72; Conservative 51; Mismatches 98; Indels 34; Gaps 12;
 Q0 5 KVKVKMFFVLTPLGLTISQEVFAQDPPSOLHRSVNLQNYTYEGDPVTHEN 64
 Q0 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Q0 2 KKNIKIKIVLIVLSPILPKSKD1SNVK-----SPDLYATITPYD1KN 53
 Q0 65 VKSYDQIISHHILYNNSGPNYD---KLTTELKNOEMATLFDKNDV1DGYEYH1CYLC 120
 Q0 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Q0 54 CR-VNFSTHTL--NDTORYGRKDYYIISSEMASOKFKEDDHYDVFGL-FVIL--- 105
 Q0 DB 121 ENAERACIYGGT--NHEGNHLEIHKVVKVYSIDG--I0SLSDIETNKMVTAQEL 175
 Q0 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Q0 106 -NSHTGEYIYGITPAQNNKVNH---KLLGNFLFISQESQNLANKKILLEKD1V7QEI 159
 Q0 176 DYKTRYLTDNKOLYTNGSKYETGYIKF1PKNEKSEFDFPEP-EFTQSKEYLMIYKDN 234
 Q0 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Q0 160 DFKTRYLMDNYK1Y-DATSPVSGR1E7GKDSQHCEQIDLFDSPNEGTRSDIFAKYKDN 218

Oy 235 ETLD-SNTSQIEVYL 248
 Oy 219 RIINMKNFNSHFDIVL 233

Db RESULT 11
 SPEH_STREP STANDARD; PRT; 236 AA.
 ID SPEH_STREP
 AC Q9XIC8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Exotoxin type H precursor (SPE_H).
 GN SPEH OR SP1108.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus
 NCBI_TAXID=1314;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=M15;
 RC MEDLINE=9903438; PubMed=9874566;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Profit T.; Moffatt S.L.; Berkahn C.J.; Fraser J.D.;
 RA Primeaux C.; Sezate S.; Surov A.N.; Kenton S.; Iai H.S.; Lin S.P.;
 RA Qian Y.; Jia H.G.; Najar F.Z.; Ren Q.; Zhu H.; Song L.; White J.;
 RA Yuan X.; Clifton S.W.; Roe B.A.; McLaughlin R.;
 RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta chain.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
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 CC
 DR EMBL; AF124500; AF030999.1; .
 DR EMBL; AB006546; AAK33907.1; .
 DR PDB; 11ET9; 24-MAY-00.
 DR PDB; 1EN4; 24-MAY-00.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph/tox_OB.
 DR Pfam; PF02876; Staph/Strep_tox_C; 1.
 DR Pfam; PF01123; Staph/Strep_toxin; 1.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR KW Toxin; Signal; Complete proteome; 3D-structure.
 FT SIGNAL 1
 FT CHAIN 32
 DR SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;
 DR
 DR Query Match 16.1%; Score 213.5; DB 1; Length 236;
 DR Best Local Similarity 29.3%; Pred. No. 2.3e-09;
 DR Matches 72; Conservative 38; Mismatches 113; Indels 23; Gaps 9;
 DR
 DR 8 LKKMVFVFLYELGTLISQEVFAQDQDPSPQLHRSVNLQNYTYEGDPVTHEN 67

10	1DKKYSMLICLSPFLSYRNQANSYNTNRHNLSELYKHDNSN--LLEADSTKNN--S	62	DR PRINTS; PRO0279; BACTRILTOXIN.
68	VDQLLSHLIVNNSGPNYDKLTELKNOEMMATEFKDKVNDIYGVYHHLCYLCENAERSA	127	DR PROSTE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
63	PDIVTSHMLKSYKDKN--LSVFEFKWISQEFKDKVDTIVSAAQEVCE-CPGKRYEA	118	DR PROSTE; PS00278; STAPH_STREP_TOXIN_2; 1.
128	CIYGGV--TNHGNHLETPKPKIVKVSIDGQISSLSEFDETKNKRMTVQAGLDYKVRKYLT	185	KW Toxin; Signal; Complete proteome.
119	--FPGITLTNSEKEKIP--VNWDKSKQQPMPFTVVKPKVTAQEVDIKVRKLJL	172	FT SIGNAL 1
186	NKOLYTNGPSKTYGTGKFKPKNKEKFED--FPEPEPEFTOSKYLMIYKDNENFLDSNTSQ	243	FT CHAIN 24 POTENTIAL.
173	KYDLYNNREQQKYSKGTVTLDLNGSKD1VFDLYYFGNGDF--NSMLK1YSNNERIDSTQFH	230	FT SEQNCE 234 EXOTOKIN TYPE G.
244	IEVYLT 249		FT SEQNCE 234 AA; 4955C49E4BA2052 CRC64;
231	VDTSIS 236		63 ENVKSVDQLLSHLIVNNSGPNYDK--LKTLEKNOEMA-----
Qy			99 -TLFKDKNDIYGVYHHLCYLCENAERSACIYGGTNH--EGNHLEIPKIVVWSIDG 155
Db			64 DQF1RQDKDVYFGPKYFNSPPYVDN----IYGIVVKHNSQGNK--SIQFVGTLNQDG 134
Qy			84 DQF1RQDKDVYFGPKYFNSPPYVDN----IYGIVVKHNSQGNK--SIQFVGTLNQDG 134
Db			85 IQSL--SFDETNKMKVTAQELDKVRYLTDNQKLYTNGPSKTYGTGKFKPKNNEVS 213
Qy			156 IQSL--SFDETNKMKVTAQELDKVRYLTDNQKLYTNGPSKTYGTGKFKPKNNEVS 213
Db			135 KETYLPSAETRKKKQFTLQEFDFKFRKFLMEKYNN-DSESRYSIGSLFLATKSKHYE 193
Qy			214 FDFEPEPE--FTOSKYLMIYKDNENFLDS-NTSQUEVYLT 250
Db			194 VDLFNRDDKLRSDFKRYKDKN1FNSNEETSHDDYLKT 233
RESULT 13			
		TSST_STAAU	STANDARD; PRT; 234 AA.
		ID TSST_STAAU	
		AC P06686;	
		DT 01-JAN-1988 (Rel. 06, Created)	
		DT 01-JAN-1988 (Rel. 06, Last sequence update)	
		DT 28-FEB-2003 (Rel. 41, Last annotation update)	
		DE Toxin-1 precursor (TSST-1).	
		GN TST.	
		OS Staphylococcus aureus.	
		OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae;	
		OX NCBI_TaxID=1280;	
		RN [1]	
		RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
		RX MEDLINE=87057222; PubMed=3782090;	
		RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,	
		RA Schlievert P.M.;	
		RA "The nucleotide and partial amino acid sequence of toxic shock	
		RT syndrome toxin-1,"	
		RT J. Biol. Chem. 261:15783-15786 (1986).	
		RN [2]	
		RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).	
		RX MEDLINE=41450598; PubMed=8107781;	
		RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,	
		RA Brehm R.D., Tranter H.S.; "Structural basis of superantigen action inferred from crystal	
		RT structure of toxic-shock syndrome toxin-1."	
		RL Nature 367:94-97 (1994).	
		RN [4]	
		RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).	
		RX MEDLINE=96319751; PubMed=875320;	
		RA Papegeorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,	
		RA Acharya K.R.; "The refined crystal structure of toxic shock syndrome toxin-1 at	
		RT 2.07 Å resolution."	
		RT Biochemistry 32:13761-13766(1993).	
		RL J. Mol. Biol. 260:553-569(1996).	
		RN [5]	

RP	X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX	PRASADLINE=973342; PubMed=9194182;
RX	PRASAD G. S., Radhakrishnan R., Mitchell D.T., Barhart C.A.,
RA	Dinges M.M., Cook W.J., Schilhert P.M., Ohlendorf D.H.;
RA	Refined structures of three crystal forms of toxic shock syndrome
RT	Toxin-1 and of a tetramatin with reduced activity ";
RT	Protein Sci. 6:1220-1227(1997).
RL	X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
RN	PRASADLINE=9825504; PubMed=9505531;
RX	Barhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M
RA	Schilhert P.M., Ohlendorf D.H.;
RA	Structures of five mutants of toxic shock syndrome toxin-1 with
RT	reduced biological activity.;
RT	Biochemistry 37:7194-7207(1998).
RL	1--SUBCELLULAR LOCATION: Secreted.
CC	- - DISEASE: THIS TOXIN IS RESPONSIBLE FOR THE SYMPTOMS OF TOXIC
CC	SHOCK SYNDROME.
CC	- 1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCAL TOXIN
CC	FAMILY.
CC	-----
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CC	-----
CD	EMBL; J02615; AA26682.1; -.
DR	PTR; A24606; XCSAS1.
DR	PDB; 2TSS; 24-DEC-97.
DR	PDB; 3TSS; 24-DEC-97.
DR	PDB; 4TSS; 24-DEC-97.
DR	PDB; 5TSS; 24-DEC-97.
DR	PDB; 1OIL; 12-AUG-97.
DR	PDB; 2QIL; 12-AUG-97.
DR	PDB; 1AWI; 18-NOV-98.
DR	PDB; 1TS2; 16-DEC-98.
DR	PDB; 1TS3; 16-DEC-98.
DR	PDB; 1TS4; 16-DEC-98.
DR	PDB; 1TS5; 16-DEC-98.
DR	InterPro; IPR006123; Staph/Strep_toxin.
DR	InterPro; IPR006126; Staph/Strep_tox.
DR	InterPro; IPR006173; Staph_tox_OB.
DR	InterPro; IPR006125; Staph_toxin.
DR	Pfam; PF02876; Staph_Strp_tox_C; 1.
DR	Pfam; PF01123; Staph_Strp_toxin; 1.
DR	PRINTS; PRO1551; TOXICSS_TOXIN.
DR	PROSITE; PS00077; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
WT	Toxin; Superantigen; Signal; 3D-structure.
WT	SIGNAL 1 40 TOXIC SHOCK SYNDROME TOXIN-1.
WT	CHAIN 1 234
WT	HELIX 4 1
WT	SPRAND 4 54
WT	TURN 5 69
WT	SPRAND 58 71
WT	SPRAND 72 76
WT	TURN 78 79
WT	SPRAND 82 86
WT	TURN 91 91
WT	SPRAND 98 99
WT	SPRAND 101 108
WT	SPRAND 113 114
WT	TURN 116 117
WT	SPRAND 120 125
WT	SPRAND 128 129
WT	SPRAND 133 138
WT	SPRAND 142 146
WT	TURN 147 148
WT	SPRAND 149 151
WT	SPRAND 159 161
WT	SPRAND 163 164

FT	HELIX	166	181
FT	TURN	183	185
FT	TURN	187	188
FT	STRAND	192	198
FT	TURN	199	200
FT	STRAND	203	207
FT	TURN	208	209
FT	HELIX	214	216
FT	STRAND	221	222
FT	HELIX	223	225
FT	STRAND	226	234
SQ	SEQUENCE	234 AA:	26306 MW: E95789FF9A1D7AB4 CRC64;
Query Match		8 8%	Score 116; DB 1; Length 234;
Best Local Similarity		23.7%	Prd. No. 0.056;
Matches 5;	Conservative	35;	Mismatches 107; Indels 42; Gaps 8;
Qy	4	NKKVLLKKMVFVYFLVFLGLTISQEVAQQODPDSLHRSSLYK-----NLQNIYFLY 55	
Db	2	NKKL - MNFFIVSPILLATTA -----TDETPPLSSNQIYKATASTDNDKIDLDWY 53	
Qy	56	EGDEPVTHENVKSDVOLLSHLITYNVSG-----PNYDKLKLTKLNQEMATLFDKRNV 106	
Db	54	SGSGSDTFTNSEVLDNSLGSMRKNTDGSISLIIIFSPSPYSPATFKGEKVDLNTKRTKKSQ 113	
Qy	107	DTIGVEYYHLCLCNAERSACTYYGTYNIEGNEGLIEPKKIVKVKVTDGQQS-LSFDEIET 165	
Db	114	HTSEGTYIHF-----QISGYTNT-E-KLPTPIELPKVKGDKSPLIKYGPKF 159	
Qy	166	NKRMVTAQELDKVVKYLTDNKLQYLTGPKSYKETGYKTFPKNEKSFWFDFPEPEFQGS 225	
Db	160	DKKRLAATSTLDFEIRQLTQIHLGRS--SDKTYGKWTIMDGSTYQSDLSKRFEINTE 217	
Qy	226	K 226	
Db	218	K 218	
RESULT 14			
USO1_YEAST			
ID	USO1_YEAST	STANDARD;	PRT; 1790 AA.
AC	P25386;		
DT	01-MAY-1992 (Rel. 22)	Created	
DT	01-MAY-1992 (Rel. 22)	Last sequence update	
DT	16-oct-2010 (Rel. 40)	Last annotation update	
DE	Intracellular protein		
DE	USO1 OR INT1 OR YD1058W	Transport protein USO1.	
GN			
OS	Saccharomyces cerevisiae (Baker's yeast)		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes;		
OC	Saccharomycetales; Saccharomyctaceae; Saccharomyces.		
OX	NCBI_TaxID=4932;		
RN	[1]	SEQUENCE FROM N.A.	
RP			
RC	STRAIN=X2180-1A;		
RX	MEDLINE=91185402; PubMed=2010462;		
RA	Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K., Yamamoto M.;		
RT	"A cytoskeleton related gene, uso1, is required for intracellular protein transport in Saccharomyces cerevisiae."		
RT	[2]	SEQUENCE OF 782-1790 FROM N.A.	
RA	Hosstetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N., Kendrick K.E.; Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.		
RN	[3]	SEQUENCE OF 1-8 FROM N.A.	
RA	Bai Y., Symington L.S.;		
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI COMPLEX.		
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE		
CC	-1- MEMBRANES.		

CC ER AND THE GOLGI COMPLEX.
 CC -1 DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED
 CC OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL
 CC COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.
 CC -1 SIMILARITY: BELONGS TO THE VDP/US01/YBL047C FAMILY.

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DR EMBL: X54378; CAA38253.1; -;
 DR EMBL: L03188; AAB00143.1; -;
 DR EMBL: U536668; AAB66659.1; -;
 DR SGD; S0002216; US01.
 DR InterPro; IPR02017; Spectrin.
 DR InterPro; IPR006955; Us01_p115_C.
 DR InterPro; IPR006954; Us01_p115_head.
 DR Pfam; PF04871; Us01_p115_C; 1.
 DR Pfam; PF04869; Us01_p115_head; 1.
 KW Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.
 FT DOMAIN 1 724 GLOBULAR HEAD.
 FT DOMAIN 1 725 1790 COILED COIL (POTENTIAL).
 FT DOMAIN 1 465 487 CHARGED (HYPER-HYDROPHILIC).
 FT DOMAIN 1 991 1790 DISPENSABLE FOR THE PROTEIN FUNCTION.
 FT DOMAIN 1 1172 1786 ASP/GLU-RICH (ACIDIC).
 FT CONFLICT 847 847 G->E (IN REF. 2).
 FT CONFLICT 924 924 E->K (IN REF. 2).
 FT CONFLICT 1253 1253 V->I (IN REF. 2).
 FT CONFLICT 1319 1319 I->V (IN REF. 2).
 FT CONFLICT 1461 1461 N->S (IN REF. 2).
 FT CONFLICT 1581 1581 G->S (IN REF. 2).
 FT CONFLICT 1600 1600 I->V (IN REF. 2).
 FT CONFLICT 1661 1661 R->S (IN REF. 2).
 FT CONFLICT 1772 1772 D->DEEDEE (IN REF. 2).
 SQ SEQUENCE 1 90 AA: 206424 MW: 6CE2B16E9D481.8 CRC64;

Query Match 7.7% Score 102.5; DB: 1; Length 1790;
 Best Local Similarity 24.1%; Pred. No. 7;
 Matches 62; Conservative 37; Mismatches 105; Indels 53; Gaps 11;

Qy 1 MENKKVLLKMMVFPTLVTPLGLTISQEVPAQQDPDSQLHRSSL--VKALQUNIVFLYED 58
 b 1500 LEKSKEMMKLESTEESNETELKSSMETIRKSDEKLSKSAEDIKLQH---ERK 1555
 Qy 59 PVT--HENTVSKDQDLSHLLIYVNSPQYDPLKLTKE--NOEMATLFKDKNYDI 108
 Db 1556 LISRNESKEDEEKLSSKRLIEAKSGSELETVKOBINNAQEKKIRINAENTVLSKLEDI 1615
 Qy 109 YGVVEYHLCYLCENAERSACIYGGVTHNHEGNHLEPKKIVVYKSIDGIQLSFDIETNKK 168
 Db 1616 ER-----EIKDKQAEI---KSQNQEKELELTSRKELEQELDSTQ-----QKA 1654
 Qy 169 MVTAQELDKYKVRKYLTDNKQLYTNGPSKETGYIKFIPKNNKESTWDFPPEPEPTQSKYL 228
 Db 1655 QKSEEBERRAEVRKQVEKSOL-DEKAMLLETKNDLV--NKEQAW---KRDEDTVKK -- 1705

Qy 229 MIYKDNETLDSNTSQE 245
 Db 1706 -----TDSQREIE 1715

RESULT 15

ID DSC1_HUMAN STANDARD; PRT; 894 AA.

AC Q00554; DR 01-NOV-1997 (Ref. 35, Created)
 DR 01-NOV-1997 (Ref. 35, Last sequence update)
 DR 15-SEP-2003 (Ref. 42, Last annotation update)

Desmocollin 1A/1B precursor (Desmosomal glycoprotein 2/3) (DG2/DG3).

GN DSC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCB_1_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Foreskin;
 RC MEDLINE=3283249; PubMed=8507556;
 RX Thesis D.G., Koch P.J., Franke W.W.;
 RA RT "different synthesis of type 1 and type 2 desmocollin mRNAs in
 RT human stratified epithelia."
 RL Int. J. Dev. Biol. 37:101-110(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Foreskin;
 RA Zimbelmann R.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DDJB databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=34116381; PubMed=82880219;
 RA King I.A., Arnemann J.J., Spurr N.K., Buxton R.S.;
 RT "Cloning of the cDNA (DSC1) coding for human type 1 desmocollin and
 RT its assignment to chromosome 18." Genomics 18:185-194(1993).
 RL FEBS Lett. 286:9-12(1991).
 RN [4]
 RP SEQUENCE OF 135-151 AND 283-292.
 RX MEDLINE=9132353; PubMed=1713860;
 RA King I.A., Maree A.I., Rees D.A., Buxton R.S.;
 RT "Keratinization is associated with the expression of a new protein
 RT related to the desmosomal cadherins DGI/III." Genomics 18:185-194(1993).
 RL FEBS Lett. 286:9-12(1991).
 CC -1 FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS, INVOLVED
 CC IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
 CC MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL
 CC POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
 CC ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED
 CC TO THE KERATINIZATION OF EPITHELIAL TISSUES.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
 CC Name=1A; Synonyms=DG2;
 CC IsoId=Q08554-1; Sequence=Displayed;
 CC Name=1B; Synonyms=DG3;
 CC IsoId=Q08554-2; Sequence=VSP 000651; VSP_000652;
 CC -1 TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH
 CC NODE AND TONGUE.
 CC -1 DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
 CC (POTENTIAL).
 CC -1 SIMILARITY: Contains 5 cadherin domains.
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 DR EMBL: Z34522; CAA84279.1; -;
 DR EMBL: Z34522; CAA84278.1; -;
 DR EMBL: X72925; CAA51429.1; -;
 DR PIR: 137281; I37281;
 DR PIR: 137282; I37282;
 DR HSSP: P151.6; INCJ;
 DR Genew; HGNC:3035; DSC1.
 DR MIM; 125643;
 DR GO; GO:0005921; C:gap junction; TAS.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; cadherin_5.

